

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:35:48 ; Search time 11 Seconds
(without alignments)
448.891 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTSQCA.....CSRFPDGRYRCMSDLKINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 15344

Minimum DB seq length: 0

Maximum DB seq length: 105

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	589	100.0	105	1 PRK1 HUMAN	P58294 homo sapien
2	310.5	52.7	81	1 VPRA_DENPO	P25687 dendroaspis
3	287.5	48.8	96	1 BV8_BOMVA	Q9PW66 bomina var
4	78	13.2	70	1 CX2X CONBE	Q9U323 conus betul
5	66	11.2	85	1 HEPG_MORCS	P82951 morone chry
6	64.5	11.0	102	1 TXCA_CAEEX	Q8MTX1 caerostris
7	62	10.5	92	1 LCM_LOCM1	P80060 locusta mig
8	62	10.5	100	1 VP52 BPAPS	Q9T1P6 bacterioph
9	60.5	10.3	99	1 GAS3 ARATH	P46687 arabidopsis
10	60	10.2	102	1 108 LYCES	Q43495 lycopersico
11	58	9.8	46	1 ENA1 HORSE	P80930 equus cabal
12	57.5	9.8	68	1 ACTX_HADVE	P81803 hadronyche
13	57	9.7	99	1 SVS7_MOUSE	Q09098 mus musculu
14	56	9.5	78	1 MT2 MUSAC	O22119 musa acumin
15	55.5	9.4	99	1 FIL1 ANTM	Q38737 antirrhinum
16	54.5	9.3	57	1 GRN3_CYPCA	P81015 cyprinus ca
17	54.5	9.3	90	1 BXB7_BOMMO	P26741 bombyx mori
18	54	9.2	84	1 SCX9_CENSC	Q95WC9 centrurroide
19	54	9.2	87	1 SCX2_CENSC	P01493 centrurroide
20	53.5	9.1	57	1 GRN1_CYPCA	P81013 cyprinus ca
21	53.5	9.1	60	1 MTA_CYP51	Q92044 cyprinodon
22	53.5	9.1	96	1 RS11 LYCES	P47926 lycopersico
23	53	9.0	47	1 SIAL_SORBI	P21923 sorghum bic
24	53	9.0	47	1 THZ2_MAIZE	P81009 zea mays (m
25	52.5	8.9	68	1 ICE2_ASCSU	P07852 ascaris suu
26	52.5	8.9	65	1 MT_LYTRI	O02033 lytechinus
27	52.5	8.9	70	1 DMVC_DROME	P41964 drosophila
28	52.5	8.9	76	1 EC_MAIZE	P43401 zea mays (m
29	52.5	8.9	99	1 GAS2_AEATH	P46688 arabidopsis
30	52	8.8	75	1 SG8S_DROME	P02842 drosophila
31	52	8.8	90	1 OM3_CHLPP	Q9Z7Z5 chlamydia p
32	51.5	8.7	85	1 SC12_MESMA	Q9GQW3 mesobuthus
33	51.5	8.7	87	1 SCX6_CENNO	P45664 centrurroide

34 51 8.7 73 1 MT_DREPO Q94550 dreissena p
35 51 8.7 87 1 OM3_CHLPS P27606 chlamydia p
36 51 8.7 99 1 RSP1_RAT Q9GXN2 rattus norv
37 50.5 8.6 60 1 MT1_CYPCA O13269 cyprinus ca
38 50.5 8.6 62 1 MT_XENLA O05890 xenopus lae
39 50.5 8.6 90 1 LIM1_LILLO Q43533 lilium long
40 50.5 8.6 90 1 LIM2_LILLO Q43534 lilium long
41 50 8.5 66 1 MT_ARIAR P55946 arianta arb
42 50 8.5 68 1 DIS1_AGRKH P17494 agkistrodon
43 50 8.5 87 1 SCX5_CENNO P45663 centrurroide
44 49.5 8.4 47 1 TX45_PHONI P59367 phoneutria
45 49.5 8.4 73 1 DISB_TRIGA P17495 trimeresuru

ALIGNMENTS

RESULT 1
PRK1 HUMAN STANDARD; PRT; 105 AA.
AC P58294;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF) (Mambakine).
GN PROK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21160229; PubMed=11259612;
RA Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.Y.;
RT "Identification of two prokineticin cDNAs: recombinant proteins potentially contract gastrointestinal smooth muscle.";
RL Mol. Pharmacol. 59:692-698(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21419730; PubMed=11528470;
RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z., Dillard-Telm L., Frantz G., Rangell L., DeGuzman L., Keller G.-A., Peale F., Gurney A., Hillan K.J., Ferrara N.;
RT "Identification of an angiogenic mitogen selective for endocrine gland endothelium.";
RL Nature 412:877-884(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Fraser C.;
RT "Mambakine, a snake venom related endocrine hormone that controls macrophages.";
Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle. Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary, testis, adrenal and placenta.
-!- SIMILARITY: BELONGS TO THE PROKINETICIN FAMILY.
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EMBL; AF333024; AAK49918.1; -.
DR EMBL; AY029225; AAK33111.1; -.

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DR Genew; HGNC:18454; PROK1.
DR MIM; 606233; ...
KW Mitogen; Growth factor; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 105 PROKINETICIN 1.
FT FT DISULFID 26 38 BY SIMILARITY.
FT FT DISULFID 32 50 BY SIMILARITY.
FT FT DISULFID 37 78 BY SIMILARITY.
FT FT DISULFID 60 86 BY SIMILARITY.
FT FT DISULFID 80 96 BY SIMILARITY.
SQ SEQUENCE 105 AA; 11715 MW; C7E3FDE30EBF416A CRC64;

Query Match 100.0%; Score 589; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.9e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBC 60
DB 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBC 60

QY 61 HPGSHKVPFRKRGKHTCCPLNLLCSRFPDGRYRCMDLKNINF 105
DB 61 HPGSHKVPFRKRGKHTCCPLNLLCSRFPDGRYRCMDLKNINF 105

RESULT 2
VPRA_DENPO STANDARD; PRT; 81 AA.
AC P25687;
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Intestinal toxin 1 (MIT 1) (MIR1) (Venom protein A).
OS Dendroaspis polylepis polylepis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI_TaxID=8620;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RX MEDLINE=81115818; PubMed=7461607;
RA Joubert F.J., Strydom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
RT polylepis polylepis (black mamba) venom.";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=20036442; PubMed=10567694;
RA Schweitz H., Pascaud P., Diehot S., Moinier D., Lazdunski M.;
RT "MIR1, a black mamba toxin with a new and highly potent activity on
RT intestinal contraction.";
RL FEBS Lett. 461:183-188(1998).
RN [3]
RP STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=98437381; PubMed=9761684;
RA Boissouvier J., Albrand J.-P., Blackledge M., Jaquinod M.,
RA Schweitz H., Lazdunski M., Marion D.;
RT "A structural homologue of colipase in black mamba venom revealed by
RT NMR floating disulphide bridge analysis.";
RL J. Mol. Biol. 283:205-219(1998).
CC -|- FUNCTION: Potentially contract gastrointestinal (GI) smooth muscle.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC PDB; 1IMT; 20-APR-99.
KW Toxin; 3D-structure.
FT DISULFID 7 19
FT DISULFID 13 31
FT DISULFID 18 60
FT DISULFID 41 68
FT DISULFID 62 78
FT VARIANT 73 73 P -> Q (IN PROTEIN A').

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FT CONFLICT 18 18 C -> S (IN REF. 1).
FT CONFLICT 22 22 S -> C (IN REF. 1).
SQ SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;

Query Match 52.7%; Score 310.5; DB 1; Length 81;
Best Local Similarity 62.8%; Pred. No. 1.7e-25;
Matches 49; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 20 AVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBCPGSHKVPFRKRGK-HHTC 78
DB 1 AVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBCPGSHKVPFRKRGK-HHTC 78

QY 79 PCPLNLLCSRFPDGRYRC 96
DB 61 PCAPNLCVQTSPPKFKC 78

RESULT 3
BV8_BOMVA STANDARD; PRT; 96 AA.
AC Q9P866;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein Bv8 precursor.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=99349621; PubMed=10422759;
RA Mollay C., Wehselberger C., Mignogna G., Negri L., Melchiorri P.,
RA Barra D., Kreil G.;
RT "Bv8, a small protein from frog skin and its homologue from snake
RT venom induce hyperalgesia in rats.";
RL Eur. J. Pharmacol. 374:189-196(1999).
CC -|- FUNCTION: Potentially contract gastrointestinal (GI) smooth muscle.
CC -|- Induces hyperalgesia.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE PROKINETICIN FAMILY.
CC -----
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CC -----
DR EMBL; AF168790; RAD45816.1; -.
DR HSSP; P25687; 1IMT.
KW Signal.
FT SIGNAL 1 19 PROTEIN BV8.
FT CHAIN 20 96 BY SIMILARITY.
FT DISULFID 26 38 BY SIMILARITY.
FT DISULFID 32 50 BY SIMILARITY.
FT DISULFID 37 78 BY SIMILARITY.
FT DISULFID 60 86 BY SIMILARITY.
FT DISULFID 80 95 BY SIMILARITY.
SQ SEQUENCE 96 AA; 10102 MW; A12490A7437609B4 CRC64;

Query Match 48.8%; Score 287.5; DB 1; Length 96;
Best Local Similarity 50.5%; Pred. No. 4.5e-23;
Matches 49; Conservative 18; Mismatches 29; Indels 1; Gaps 1;

QY 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBC 60
DB 1 MKCFAGIVVLLLVIAFSGHCAVITGACDKVQCGSGTCCCAASWSNRNIRFCIPLNGSGDC 60

QY 61 HPGSHKVPFRKRGKHTCCPLNLLCSRFPDGRYRC 97
DB 61 HPGSHKVPFRKRGKHTCCPLNLLCSRFPDGRYRC 97
```

Db 61 HPASHKVPYDGRKRLSLCPCKSLGTCCKSGE-KFKCS 96

RESULT 4
CX2X_CONBE STANDARD; PRT; 70 AA.

AC Q9U323;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conotoxin beta precursor.
OS Conus betulinus (Beech cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89764;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct;
RA Fan C.-X.;
RT "A conotoxin with novel cysteine framework from Conus betulinus of south China sea";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
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CC
CC EMBL; AF208661; AAF23167.1; -
KW Neurotoxin; Toxin; Signal; Amidation;
KW Cleavage on pair of basic residues.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 57 CONOTOXIN BETA.
FT PROPEP 61 70
FT MOD_RES 57 57
FT SEQUENCE 70 AA; 7900 MW; F6575A2E830AD903 CRC64;
Query Match 13.2%; Score 78; DB 1; Length 70;
Best Local Similarity 32.9%; Pred. No. 0.12; Indels 24; Gaps 5;
Matches 26; Conservative 5; Mismatches 24; Indels 24; Gaps 5;
SQ SEQUENCE 70 AA; 7900 MW; F6575A2E830AD903 CRC64;
QY 5 TRVSIMLLLVTSDCAVITGA-----CERDVQCGAGTCCATSLWLRGLRMCTPLGREG 57
Db 6 TSVGCLLVIVFLNVLVPTVSACRAEGTYCENDSQCLNECC-----W-----GGCG 51
QY 58 BEC-HPG--SHKVFFPRKR 73
Db 52 HPCRHPGRSKLQEFFRQR 70
RESULT 5
HEPC_MORCS STANDARD; PRT; 85 AA.
AC P82951;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepsicidin precursor.
OS Morone chrysops x Morone saxatilis (White bass x Striped bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Morone.
OX NCBI_TaxID=45352;
RN [1]
RP SEQUENCE FROM N.A.; SEQUENCE OF 65-85, TISSUE SPECIFICITY, AND

RP ANTIBIOTIC ACTIVITY.
RC TISSUE=Gill, and Skin;
RX MEDLINE=21982021; PubMed=11985602;
RA Shike H., Lauth X., Westerman M.E., Ostland V.E., Carlberg J.M.,
RA Van Olst J.C., Shimizu C., Bulet P., Burns J.C.;
RT "Bass hepcidin is a novel antimicrobial peptide induced by bacterial challenge";
RL Eur. J. Biochem. 269:2232-2237(2002).
CC -!- FUNCTION: Seems to act as a signaling molecule involved in the maintenance of iron homeostasis. Seems to be required in conjunction with HFE to regulate both intestinal iron absorption and iron storage in macrophages (By similarity).
CC -!- FUNCTION: Antimicrobial activity against Gram-negative bacteria such as E.coli.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in liver.
CC -!- INDUCTION: By bacterial challenge.
CC -!- MASS SPECTROMETRY: MW=2255.97; METHOD=MALDI; RANGE=65-85.
CC -!- SIMILARITY: BELONGS TO THE HEPICIDIN FAMILY.
CC
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CC
CC EMBL; AF394246; AAM28440.1; -
KW Antibiotic; Hormone; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 64
FT CHAIN 65 85 HEPICIDIN.
FT DISULFID 66 72 POTENTIAL.
FT DISULFID 69 83 POTENTIAL.
FT DISULFID 70 82 POTENTIAL.
FT DISULFID 73 79 POTENTIAL.
SQ SEQUENCE 85 AA; 9484 MW; 0FEA55CF0A522C84 CRC64;
Query Match 11.2%; Score 66; DB 1; Length 85;
Best Local Similarity 30.0%; Pred. No. 2.4; Indels 12; Gaps 2;
Matches 15; Conservative 8; Mismatches 15; Indels 12; Gaps 2;
QY 52 PLGREGEGCHPGSHKVPFFRKRKHT-----CPCLPNL-----LCGRF 89
Db 36 PMSNEYQEMPVSWPYNNRHKRSSPGCFCCNCCPNMSGCGVCCRF 85
RESULT 6
TXCA_CAEEX STANDARD; PRT; 102 AA.
AC Q8MTX1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurotoxic peptide caeron precursor.
OS Caerostris extrusa (Bark spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Araneidae; Caerostris.
OX NCBI_TaxID=172846;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Dai L., Naoki H., Nakajima T.;
RT "cDNA sequence of neurotoxic peptide, caeron, from spider Caerostris extrusa venom";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
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CC -----
DR EMBL; AY050523; AAL12487.1; -;
KW Toxin; Neurotoxin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 102 NEUROTOXIC PEPTIDE CABRON.
SQ SEQUENCE 102 AA; 11403 MW; C351E1287F837C52 CRC64;

Query Match 11.0%; Score 64.5; DB 1; Length 102;
Best Local Similarity 29.7%; Pred. No. 4;
Matches 19; Conservative 10; Mismatches 30; Indels 5; Gaps 4;

QY 24 GACERDVQAGTCCATSAISLWRLGRLMCTPLGREGEC-HPGSHKVPFFRKRRKHHHTCPCLP 82
DB 23 GDCCKNSDCKAGGCC-VNTPPFARSTCKYLOQGEFCAMGKYN-PL--GKVINMPCGK 78

QY 83 NLLC 86
DB 79 GLKC 82

RESULT 7

LCM_LCMCI STANDARD; PRT; 92 AA.
AC P80060; F80058;
DT 01-MAR-1992 (Rel. 21, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protease inhibitors precursor (Contains: Protease inhibitor LCMCI I
DE (PARS intercerebralis major peptide D2) (PMP-D2); Protease
DE inhibitor LCMCI II (PARS intercerebralis major peptide C) (PMP-C)).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;

[1] SEQUENCE FROM N.A.

RP TISSUE=Fat body;

RC Lagueux M.L.;

RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.

[2] SEQUENCE OF 1-16 FROM N.A.

RP TISSUE=Fat body;

RC MEDLINE=94290521; PubMed=8019577;

RA Kromer E., Nakakura N., Lagueux M.;

RT "Cloning of a Locusta cDNA encoding a precursor peptide for two

RT structurally related proteinase inhibitors.";

RL Insect Biochem. Mol. Biol. 24:329-331(1994).

[3] SEQUENCE OF 20-54 AND 57-92.

RP TISSUE=Fat body;

RC MEDLINE=92155197; PubMed=1740125;

RA Nakakura N., Hietter H., van Dorsselaer A., Luu B.;

RT "Isolation and structural determination of three peptides from the

RT insect Locusta migratoria. Identification of a deoxyhexose-linked

RT peptide.";

RL Eur. J. Biochem. 204:147-153(1992).

[4] SEQUENCE OF 20-54 AND 57-92.

RP TISSUE=Hemolymph;

RC MEDLINE=93112047; PubMed=1472051;

RA Boigegrain R.-A., Mattas H., Brehelin M., Paroutaud P.,

RA Coletti-Previero M.-A.;

RT "Insect immunity: two proteinase inhibitors from hemolymph of Locusta

RT migratoria.";

RL Biochem. Biophys. Res. Commun. 189:790-793(1992).

[5] STRUCTURE BY NMR OF LCMCI-I.

RP MEDLINE=95101633; PubMed=7803403;

RA Mer G., Kellenberger C., Koehl P., Stote R., Sorokine O.,
RA van Dorsselaer A., Luu B., Hietter H., Lefevre J.-F.;
RT "Solution structure of PMP-D2, a 35-residue peptide isolated from the
RT insect Locusta migratoria.";
CC Biochemistry 33:15397-15407(1994).
RN [6]
RN STRUCTURE BY NMR OF LCMCI-II.
RX MEDLINE=96133728; PubMed=8548454;
RA Mer G., Hietter H., Lefevre J.-F.;
RT "Stabilization of proteins by glycosylation examined by NMR analysis
RT of a fucosylated proteinase inhibitor.";
RL Nat. Struct. Biol. 3:45-53(1996).
RN [7]
RN STRUCTURE BY NMR OF LCMCI-II.
RX MEDLINE=96200387; PubMed=8613985;
RA Mer G., Hietter H., Kellenberger C., Renatus M., Luu B.,
RA Lefevre J.-F.;
RT "Solution structure of PMP-C: a new fold in the group of small serine
RT proteinase inhibitors.";
RL J. Mol. Biol. 258:158-171(1996).
CC -!- FUNCTION: BOTH LCMCI I AND II ARE INHIBITORS OF CHYMOTRYPSIN AND
CC ELASTASE (IN VITRO). THEY BOTH INHIBIT THE PROPHENOL OXIDASE
CC ACTIVATION CASCADE.
CC -!- TISSUE SPECIFICITY: BRAIN AND FAT BODY.
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CC -----
DR EMBL; 222805; CA80462.1; -;
DR PIR; S36658; S36658.
DR PDB; 1PMC; 29-JAN-96.
DR PDB; 1GL0; 28-NOV-01.
DR PDB; 1GL1; 28-NOV-01.
DR Pfam; PF05375; Pacifastin_I_2.
KW Serine protease inhibitor; Signal; Glycoprotein; 3D-structure;
KW Cleavage on pair of basic residues; Repeat.
FT SIGNAL 1 19
FT PEPTIDE 20 54 PROTEASE INHIBITOR LCMCI-I.
FT PEPTIDE 57 92 PROTEASE INHIBITOR LCMCI-II.
FT DISULFID 23 38 BY SIMILARITY.
FT DISULFID 33 51 BY SIMILARITY.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 60 75
FT DISULFID 70 89
FT DISULFID 73 84
FT CARBOHYD 65 65
FT TURN 62 63
FT STRAND 66 66
FT STRAND 72 75
FT TURN 79 80
FT STRAND 82 85
SQ SEQUENCE 92 AA; 9760 MW; 2A53F9E3D97D290A CRC64;

Query Match 10.5%; Score 62; DB 1; Length 92;
Best Local Similarity 29.6%; Pred. No. 6.6;
Matches 21; Conservative 6; Mismatches 38; Indels 6; Gaps 2;

QY 10 MLLLYTVSDCAVITGACERDVQAGTCCATSAISLWRLGRLMCTPLGREGEC-HPGSHKVPF 69
DB 11 VLLVVLVQAEKCTPGQVKQDCTCTCTPTGVMGCTRGKQCPAKRE-ISCPEGK----- 64
QY 70 FRKRKHHTCP 80
DB 65 TFKDKNTCRC 75

RESULT 8
VP52_BPAPS


```

ID VF52 BPAPS STANDARD; PRT; 100 AA.
AC Q9TIP6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative protein P52.
GN 52.

OS Bacteriophage APSE-1.
VIRUSES; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OC NCBI_TaxID=106199;
OX (1)_TaxID=106199;
RN SEQUENCE FROM N.A.
RX MEDLINE=99420383; PubMed=10489345;
van der Wilk F., Dulleman A.M., Verbeek M., van den Heuvel J.F.J.M.;
RT "Isolation and characterization of APSE-1, a bacteriophage infecting
the secondary endosymbiont of acyrthosiphon pisum.";
RL Virology 262:104-113 (1999).
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF157835; AAF03995.1;
DR HSP; P25687; 11MT.
KW Hypothetical protein.
SQ SEQUENCE 100 AA; 10824 MW; 7D3B615687F8BAD2 CRC64;

Query Match 10.5%; Score 62; DB 1; Length 100;
Best Local Similarity 22.8%; Pred. No. 7.2;
Matches 18; Conservative 7; Mismatches 28; Indels 26; Gaps 2;

QY 33 GAGTCAISLWGLRMCTPLREGEGCHPGSHKVPFFRKRKHHTCP----- 79
DB 4 GASLNCAGSGWKSTK--SPLTSLWNTCAWAKHNPFPALQNRHCLTPGKALSGRASRPL 61

QY 80 -----CLPNLLCS 87
DB 62 RSARVAIFMAFCAPDLACS 80

RESULT 9
GAS3_ARATH STANDARD; PRT; 99 AA.
AC P46687;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gibberellin-regulated protein 3 precursor.
GN GAS3 OR A4G09600 OR T25P22.40.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,

Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
Kreiss M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandenbussche F.,
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirks W.,
RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
Berneiser S., Hempel S., Feldpausch M., Lamberth S., van den Daele H.,
De Keyser A., Buyshaert C., Gielen J., Villarroel R., De Clercq R.,
Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
Clark L., Doggett J., Hall S., Kay M., Lennard N., McClay K., Mayes R.,
Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
Borkova D., Bloeker H., Schaefer M., Grimm M., Loehner T.-H.,
Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Farmann B., Granderath K., Dauner D., Herzl A.,
Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
Chedof F., Cooke R., Berger C., Monfort A., Casacuberta E.,
Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
Periz-Perez A., Fumelle B., Bent E., Johnson S., Tacon D., Jesse T.,
Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,
Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
Antonov B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana.";
RL Nature 402:769-777 (1999).
CC -!- FUNCTION: INVOLVED IN LATE STAGES OF SEED MATURATION, OR IN EARLY
STEPS OF GERMINATION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: SILIQUES AND DRY SEEDS.
CC -!- PTM: SIX DISULFIDE BONDS MAY BE PRESENT.
CC -!- SIMILARITY: BELONGS TO THE GAS1 FAMILY.
CC -----
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CC -----
CC EMBL; U11764; AAB06308.1;
DR EMBL; AL161515; CAB78083.1;
DR EMBL; AL161831; CAB82127.1;
DR PIR; S60231; S60231.
DR InterPro; IPR003854; GASA.
DR Pfam; PF02704; GASA; 1.
KW Multigene family; Signal.
FT SIGNAL 1..18
FT CHAIN 1..19
SQ SEQUENCE 99 AA; 10704 MW; 84549B74B08A47FA CRC64;

Query Match 10.3%; Score 60.5; DB 1; Length 99;
Best Local Similarity 23.5%; Pred. No. 10;
Matches 27; Conservative 9; Mismatches 34; Indels 45; Gaps 7;
```

```
QY 6 RVSIMLLV-----TVSDCAVITGACERDVQCGA---GTCCAIS---LWLRLG 47
Db 5 RSTLVLLILFLCUTTELHVAHAEQVGVVVK--IDCGRGKGRCSKSSPNLCLRAC 62
QY 48 RM-----CPTLGREGECHPGSHKVPFFPKRKHHTCPCPLPNLLCSRFPDGRYRC 96
Db 63 NSCCYRCNCVFPGTAG-----NHLCPCVASITTR---GGRLKC 98

RESULT 10
108 LYCES
ID 108 LYCES STANDARD; PRT; 102 AA.
AC Q43495;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein 108 precursor.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv VF36; TISSUE=Anther;
RX MEDLINE=94143497; PubMed=8310077;
RA Chen R., Smith A.G.;
RT "Nucleotide sequence of a stamen- and tapetum-specific gene from
RT Lycopersicon esculentum.";
RL Plant Physiol. 101:1413-1413(1993).
CC -!- TISSUE SPECIFICITY: STAMEN- AND TAPETUM-SPECIFIC.
CC -!- SIMILARITY: BELONGS TO THE A9 / F1L1 FAMILY.
CC
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CC
CC EMBL; Z14088; CAA78466.1; --
DR PIR; S26409; S26409.
DR InterPro; IPR003612; AAI.
DR Pfam; PF00234; trypan_alpha_aml1; 1.
DR SMART; SM00499; AAI; 1.
DR KEGG; S00000; AAI; 1.
FT SIGNAL.
FT CHAIN.
FT PROTEIN.
FT CHAIN 1 30 POTENTIAL.
FT CHAIN 31 102 PROTEIN 108.
FT DISULFID 41 77 BY SIMILARITY.
FT DISULFID 51 66 BY SIMILARITY.
FT DISULFID 67 92 BY SIMILARITY.
FT DISULFID 79 99 BY SIMILARITY.
FT DISULFID 102 AA; CFBAA12131C3A5B92 CRC64;
SQ SEQUENCE 102 AA; 10576 MW; 10576 MW; 10576 MW; 10576 MW; 10576 MW;

Query Match 10.2%; Score 60; DB 1; Length 102;
Best Local Similarity 25.5%; Pred. No. 12;
Matches 25; Conservative 7; Mismatches 30; Indels 36; Gaps 5;

QY 9 IMLLTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGE-----ECHPG 63
Db 20 LLLLVVLOSQVI--ECQQSQCTAS-----LTGLNVCAFLVPGSPPTASTTECCNA 69
QY 64 SHKVPFFRKRKHHTCPC-----LNLICS 87
Db 70 VQSI-----NHDGMCNTWRIAQAIPAQCNLPPLSCS 100

RESULT 11
ENAL_HORSE
ID ENAL_HORSE STANDARD; PRT; 46 AA.
AC P80930;
DT 01-NOV-1997 (Rel. 35, Created)
```

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Antimicrobial peptide enAP-1 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RC TISSUE=Neutrophils;
RX MEDLINE=92347972; PubMed=1639474;
RA Couto A.M., Harwig S.S.L., Cullor J.S., Hughes J.P., Lehrer R.I.;
RT "Identification of enAP-1, an antimicrobial peptide from equine
RT neutrophils.";
RL Infect. Immun. 60:3065-3071(1992).
CC -!- FUNCTION: HAS ANTIMICROBIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC -!- SIMILARITY: SEEMS TO CORRESPONDS TO GRANULIN 7.
CC -!- SIMILARITY: SEEMS TO CORRESPONDS TO GRANULIN 7.
DR PIR; A44794; A44794.
DR InterPro; IPR001118; Granulin.
DR Pfam; PF00396; granulin; 1.
DR SMART; SM00277; GRAN; 1.
DR PROSITE; PS00799; GRANULINS; PARTIAL.
KW Antibiotic.
FT NON TER 46
SQ SEQUENCE 46 AA; 4888 MW; 2171934C15265862 CRC64;

Query Match 9.8%; Score 58; DB 1; Length 46;
Best Local Similarity 33.3%; Pred. No. 8;
Matches 17; Conservative 3; Mismatches 23; Indels 8; Gaps 2;

QY 29 DVQCGAGTGCCAISLWLRGLRMCTPLGREGECHPGSHKVPFFPKRKHHTCP 79
Db 1 DVQCGEGHFC-----HDXQTCRASQGGXACCPYSQGVCCADQR--HCCP 43

RESULT 12
ACTX_HADVE
ID ACTX_HADVE STANDARD; PRT; 68 AA.
AC P81803;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Atracotoxin-Hvf17 (ActX-Hvf17).
OS Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
OS versutus).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Hexathelidae; Hadronyche.
OX NCBI_TaxID=6904;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=20132514; PubMed=10669030;
RA Szeto T.H., Wang X.-H., Smith R., Connor M., Christie M.J.,
RA Nicholson G.M., King G.F.;
RT "Isolation of a funnel-web spider polypeptide with homology to mamba
RT intestinal toxin 1 and the embryonic head inducer Dickkopf-1.";
RL Toxicon 38:429-442(2000).
CC -!- FUNCTION: Might aid in digestion of H.versuta prey. Not toxic to
CC insects or mammals.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- PTM: Five disulfide bonds are present.
SQ SEQUENCE 68 AA; 7564 MW; E9B6C345A6E5B8CF CRC64;

Query Match 9.8%; Score 57.5; DB 1; Length 68;
Best Local Similarity 29.4%; Pred. No. 14;
Matches 20; Conservative 8; Mismatches 19; Indels 21; Gaps 5;

QY 26 CERDVQCGAGTCCAISLWLRGLRMCTPLGREGE-----HPGSHKVPFFPKRKHHTC 78
Db 3 CGDDV-CGAGHCCEYPMH-----CKRVGQVLDLCMASKATKNSGNHL--FF-----C 48
```

```
QY 79 PCLPNLLC 86
Db 49 PCDEGYMC 56

RESULT 13
SVS7 MOUSE STANDARD; PRT; 99 AA.
ID SVS7 MOUSE STANDARD; PRT; 99 AA.
AC Q09038; Q9018;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Seminal vesicle protein 7 precursor (SVS VII) (Caltrin) (Calcium
DE transport inhibitor).
DE SVS7.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 24-41, FUNCTION, AND MASS
RP SPECTROMETRY.
RC STRAIN=CD-1; TISSUE=Seminal vesicle;
RX MEDLINE=21269209; PubMed=1118436;
RA Luo C.-W., Lin H.-J., Chen Y.-H.;
RT "A novel heat-labile phospholipid-binding protein, SVS VII, in mouse
RT seminal vesicle as a sperm motility enhancer.";
RL J. Biol. Chem. 276:6913-6921(2001).
RN [2]
RP SEQUENCE OF 24-99.
RC TISSUE=Seminal vesicle;
RX MEDLINE=93016001; PubMed=1400406;
RA Coronel C.E., Winnica D.E., Novella M.L., Lardy H.A.;
RT "Purification, structure, and characterization of caltrin proteins
RT from seminal vesicle of the rat and mouse.";
RL J. Biol. Chem. 267:20909-20915(1992).
CC -!- FUNCTION: Inhibits calcium transport into spermatozoa; it does not
CC bind directly to calcium. Binds to calmodulin. Enhances sperm
CC motility.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=8538.0; METHOD=Electrospray; RANGE=24-99.
CC -!- SIMILARITY: SOME, TO LY-6/UPAR DOMAIN.
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CC
CC EMBL: AF134204; AAD55589.1; -.
CC MGD; MGI:1930790; Sv87.
CC Calcium; Calmodulin-binding; Signal.
CC SIGNAL 1 23
CC CHAIN 24 99 SEMINAL VESICLE PROTEIN 7.
CC DISULFID 26 52 POTENTIAL.
CC DISULFID 29 37 POTENTIAL.
CC DISULFID 44 70 POTENTIAL.
CC DISULFID 74 90 POTENTIAL.
CC CONFLICT 40 40 P -> S (IN REF. 1; AA SEQUENCE AND 2).
CC CONFLICT 90 91 CC -> FG (IN REF. 2).
CC CONFLICT 96 96 C -> M (IN REF. 2).
CC CONFLICT 98 98 MISSING (IN REF. 2).
CC SEQUENCE 99 AA; 11068 MW; 18DEC97C0801E84 CRC64;

Query Match 9.7%; Score 57; DB 1; Length 99;
Best Local Similarity 22.8%; Pred. No. 23;
Matches 26; Conservative 15; Mismatches 33; Indels 40; Gaps 6;

QY 1 MRGATRVSMILLVTVSDCAV---ITGACE--RDVQC--GAGTCCCAISLWRLGLRMCPTPL 53
Db 1 MNSVTKISTLLVILSFLCFVGLGNCSCSEKSRDSRCTMPQSRCA----- 46

QY 54 GREGECHPGSHKV-----PFRKPKKHT-----CPCILPNLLCSRF 89
Db 47 -KPGESCSTVSHFVGTKHVYSKQMCSPQCKEQKLTGKLLIYMCKEKNLCNSF 99

RESULT 14
MT2 MUSAC STANDARD; PRT; 78 AA.
ID MT2 MUSAC STANDARD; PRT; 78 AA.
AC Q22119;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Metallothionein-like protein type 2.
DE Metallothionein-like protein type 2.
DE Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Grand nain; TISSUE=Fruit flesh;
RX MEDLINE=98002325; PubMed=9342866;
RA Clendenen S.K., May G.D.;
RT "Differential gene expression in ripening banana fruit.";
RL Plant Physiol. 115:463-469(1997).
CC -!- FUNCTION: METALLOTHIONEIN HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
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CC
CC EMBL: AF001525; AAB82774.1; ALT INIT.
CC InterPro; IPR000347; Metallothion_15.
CC Pfam; PF01439; Metallothio_2; 1.
CC ProDom; PD001611; Metallothion_15; 1.
CC Metal-binding; Metal-thiolate Cluster.
CC SEQUENCE 78 AA; 7790 MW; 378B3EABDC217A98 CRC64;

Query Match 9.5%; Score 56; DB 1; Length 78;
Best Local Similarity 44.0%; Pred. No. 23;
Matches 11; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 32 CGAGTCCCAISLWRLGLRMCPTPLGRE 56
Db 8 CGCGSSCSGCGCGGCRMLTDLGER 32

RESULT 15
FILL ANTIMA STANDARD; PRT; 99 AA.
ID FILL ANTIMA STANDARD; PRT; 99 AA.
AC Q38737;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Stamen-specific protein FILL1 precursor.
DE FILL.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Lamiaceae; Antirrhinaceae; Antirrhineae;
OC Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Sippe 50;
RX MEDLINE=91375441; PubMed=1680216;
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:40:18 ; Search time 22 Seconds
(without alignments)
201.938 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVISMLLVTVSDCA.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 230231

Minimum DB seq length: 0

Maximum DB seq length: 105

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	589	100.0	105	4	US-09-996-243-371
2	589	100.0	105	4	US-09-712-529-5
3	65	11.0	77	3	US-08-866-545-2
4	59.5	10.1	74	1	US-08-543-238-2
5	59.5	10.1	74	1	US-08-420-526-2
6	58	9.8	93	1	US-08-464-339A-13
7	56.5	9.6	57	1	US-07-609-716-56
8	55.5	9.4	44	1	US-08-050-319B-37
9	55.5	9.4	44	2	US-08-465-982-37
10	55.5	9.4	92	2	US-07-728-215-39
11	55.5	9.4	92	4	US-08-938-085A-39
12	55.5	9.4	92	4	US-10-072-844-39
13	54.5	9.3	92	2	US-07-728-215-41
14	54.5	9.3	92	4	US-08-938-085A-41
15	54.5	9.3	92	4	US-10-072-844-41
16	52.5	8.9	69	4	US-09-480-251-6
17	52.5	8.9	70	4	US-09-480-251-2
18	52	8.8	23	4	US-09-277-078-30
19	52	8.8	36	5	PCT-US96-01720-2
20	52	8.8	49	2	US-07-963-538B-3
21	52	8.8	50	2	US-07-963-538B-2
22	52	8.8	53	2	US-07-963-538B-1
23	52	8.8	60	3	US-08-483-503A-1
24	52	8.8	90	4	US-09-198-452A-597
25	51.5	8.7	71	6	5318899-17
26	51.5	8.7	71	6	5318899-18
27	51.5	8.7	72	1	US-07-602-847C-23

ALIGNMENTS

RESULT 1

US-09-996-243-371
; Sequence 371, Application US/09996243
; Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28

Sequence 5, Appli
Sequence 5, Appli
Sequence 32154, A
Sequence 31, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 25, Appli
Sequence 11, Appli

PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089653
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089801
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089907
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089908
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089948
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089952
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090246
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090252
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090254
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090349
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090355
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090429
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090431
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090435
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090472
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090535
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090540
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090542
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090678
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090690
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090696
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090694
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090862
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/090863
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/091360
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091478
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091544
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091519
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091626
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02

;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.8e-59;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCCTPLGREGEBC 60
Db 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCCTPLGREGEBC 60
Qy 61 HPGSHKVPFFRKXKHTCPCLPNLLCSRPDPGRYCSMDLKNINF 105
Db 61 HPGSHKVPFFRKXKHTCPCLPNLLCSRPDPGRYCSMDLKNINF 105

RESULT 2

US-09-712-529-5

;; Sequence 5, Application US/09712529

;; Patent No. 6485938

;; GENERAL INFORMATION:

;; APPLICANT: Sheppard, Paul O.

;; APPLICANT: Bishop, Paul D.

;; APPLICANT: Whitmore, Theodore E.

;; APPLICANT: Thompson, Penny P.

;; TITLE OF INVENTION: Human Zven Proteins

;; FILE REFERENCE: 99-81

;; CURRENT APPLICATION NUMBER: US/09/712.529

;; CURRENT FILING DATE: 2000-11-14

;; NUMBER OF SEQ ID NOS: 7

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 5

;; LENGTH: 105

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-712-529-5

Query Match 100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.8e-59;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCCTPLGREGEBC 60
Db 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCCTPLGREGEBC 60
Qy 61 HPGSHKVPFFRKXKHTCPCLPNLLCSRPDPGRYCSMDLKNINF 105
Db 61 HPGSHKVPFFRKXKHTCPCLPNLLCSRPDPGRYCSMDLKNINF 105

RESULT 3

US-08-866-545-2

;; Sequence 2, Application US/08866545-

;; Patent No. 6265535

;; GENERAL INFORMATION:

;; APPLICANT: Greene, Mark I.

;; APPLICANT: Murali, Ramachandran

;; APPLICANT: Takasaki, Wataru

;; TITLE OF INVENTION: PEPTIDES AND PEPTIDE

;; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR

;; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR

;; TITLE OF INVENTION: USSES

;; NUMBER OF SEQUENCES: 27

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/866.545
;; FILING DATE: 30-MAY-1997
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 009113-0004-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-493-4935
;; TELEFAX: 650-493-5556
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 77 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: No. 6265535e
US-08-866-545-2

Query Match 11.0%; Score 65; DB 3; Length 77;
Best Local Similarity 37.0%; Pred. No. 2.7;
Matches 20; Conservative 5; Mismatches 17; Indels 12; Gaps 4;

Qy 17 SDCA---VITGACERD-----VQCGAGTCCCAISLWLRGLRMCCTPLGREGECHPG 63
Db 25 SRCSSDQVETQACTREQNRICTRCPGMYCALSK-OEGCRLCAPL-----RRCRPG 73

RESULT 4

US-08-543-238-2

;; Sequence 2, Application US/08543238

;; Patent No. 5607919

;; GENERAL INFORMATION:

;; APPLICANT: Bojsen, Kirsten

;; APPLICANT: Krach, Karsten M.

;; APPLICANT: Mikkelsen, Jorn D.

;; APPLICANT: Nielsen, Klaus K.

;; TITLE OF INVENTION: Anti-Microbial Proteins

;; NUMBER OF SEQUENCES: 13

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Sandoz Agro, Inc.

;; STREET: 975 California Avenue

;; CITY: Palo Alto

;; STATE: CA

;; COUNTRY: USA

;; ZIP: 94304

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/543.238

;; FILING DATE:

;; CLASSIFICATION:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Marcus-Wyner, Lynn

;; REGISTRATION NUMBER: 34,869

;; REFERENCE/DOCKET NUMBER: 137-1078/MA

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 415/354-3588

;; TELEFAX: 415/857-1125

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 74 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-543-238-2

Query Match      10.1%; Score 59.5; DB 1; Length 74;
Best Local Similarity 23.5%; Pred. No. 11;
Matches 20; Conservative 8; Mismatches 22; Indels 35; Gaps 3;

QY 9 IMLLVTVSDCAVIT-----GACERDVQCGAGTCCAISLWLRGLRMCTPL 53
Db 10 LLLLFVAFSEMNIVTKVDGAICKKPSKFKGACGRDACE-----KAC--- 52

QY 54 GREGECHPGSHKVPFFRKHKHTC 78
Db 53 ---DQENWPGGVGVFLRCRCQSC 74

RESULT 5
US-08-420-526-2
; Sequence 2, Application US/08420526
; Patent No. 5608151
; GENERAL INFORMATION:
; APPLICANT: Bojsen, Kirsten
; APPLICANT: Kragh, Karsten M.
; APPLICANT: Mikkelsen, Jorn D.
; APPLICANT: Nielsen, Klaus K.
; TITLE OF INVENTION: Anti-Microbial Proteins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sandoz Agro, Inc.
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/420,526
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Marcus-Wyner, Lynn
; REGISTRATION NUMBER: 34,869
; REFERENCE/DOCKET NUMBER: 137-1078/WA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/354-3588
; TELEFAX: 415/857-1125
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 74 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-420-526-2

Query Match      10.1%; Score 59.5; DB 1; Length 74;
Best Local Similarity 23.5%; Pred. No. 11;
Matches 20; Conservative 8; Mismatches 22; Indels 35; Gaps 3;

QY 9 IMLLVTVSDCAVIT-----GACERDVQCGAGTCCAISLWLRGLRMCTPL 53
Db 10 LLLLFVAFSEMNIVTKVDGAICKKPSKFKGACGRDACE-----KAC--- 52

QY 54 GREGECHPGSHKVPFFRKHKHTC 78
Db 53 ---DQENWPGGVGVFLRCRCQSC 74
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Db 53 ---DQENWPGGVGVFLRCRCQSC 74

RESULT 6
US-08-464-339A-13
; Sequence 13, Application US/08464339A
; Patent No. 5747280
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, ET AL.
; TITLE OF INVENTION: Human Vascular IBP-Like Growth
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,339A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14388
; FILING DATE: 9 DEC 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-332
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 93 AMINO ACIDS
;   TYPE: AMINO ACID
;   STRANDEDNESS:
;   TOPOLOGY: LINEAR
;   MOLECULE TYPE: PROTEIN
US-08-464-339A-13

Query Match      9.8%; Score 58; DB 1; Length 93;
Best Local Similarity 27.8%; Pred. No. 20;
Matches 27; Conservative 11; Mismatches 31; Indels 28; Gaps 6;

QY 3 GATRVSIMLLVTVSDCAV---ITGAC-----ERDVQCGAGTCCAISLWLRGLRMCTPLGR 55
Db 7 GPVRAVAVVLLALCSRPAVGQNCSPCRCPDPAAPCPAG-----VSLVLDGCGCCRCVCAK 62

QY 56 E-GECHPGSHKVPFFRKHKHTCPLN--LLCSRF 89
Db 63 QLGEXCTERD-----PCDPKGLFCDYY 85

RESULT 7
US-07-609-716-56
; Sequence 56, Application US/07609716
; Patent No. 5514581
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: Functional Recombinantly Prepared
; TITLE OF INVENTION: Synthetic Protein Polymer
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
```


RESULT 8
US-08-050-3198-37
; Sequence 37, Application US/080503198
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,3198
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 37:

RESULT 10
US-07-728-215-39

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; Sequence 39, Application US/07728215
; Patent No. 5962643
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/728,215
; FILING DATE: 19910711
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8717
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-728-215-39

Query Match 9.4%; Score 55.5; DB 2; Length 92;
Best Local Similarity 26.0%; Pred. No. 38;
Matches 25; Conservative 2; Mismatches 28; Indels 41; Gaps 4;

QY 17 SDCAVITGA-CERD-----VQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
Db 6 SDFGKITGKYCECDPFCVRYKGMCSGHGQCGDCLCDSDWTGYCNC----- 56
QY 61 HPGSHKVPFRKXKHTCPCLPNLLCSRFPDGRYRC 96
Db 57 -----TRDTTCMSSNGLLCS-----GRGKC 76

RESULT 11
US-08-938-085A-39
; Sequence 39, Application US/08938085A
; Patent No. 6339148
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. 6339148el Integrin Beta Subunit and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/072,844
; FILING DATE: 06-Feb-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,085A
; FILING DATE: 26-SEP-1997
; APPLICATION NUMBER: US 07/728,215
; FILING DATE: 11-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,085A
; FILING DATE: 26-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,215
; FILING DATE: 11-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 023070-080210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-938-085A-39

Query Match 9.4%; Score 55.5; DB 4; Length 92;
Best Local Similarity 26.0%; Pred. No. 38;
Matches 25; Conservative 2; Mismatches 28; Indels 41; Gaps 4;

QY 17 SDCAVITGA-CERD-----VQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
Db 6 SDFGKITGKYCECDPFCVRYKGMCSGHGQCGDCLCDSDWTGYCNC----- 56
QY 61 HPGSHKVPFRKXKHTCPCLPNLLCSRFPDGRYRC 96
Db 57 -----TRDTTCMSSNGLLCS-----GRGKC 76

RESULT 12
US-10-072-844-39
; Sequence 39, Application US/10072844
; Patent No. 6576432
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. 6576432el Integrin Beta Subunit and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/072,844
; FILING DATE: 06-Feb-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,085A
; FILING DATE: 26-SEP-1997
; APPLICATION NUMBER: US 07/728,215
; FILING DATE: 11-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
```

;/ REFERENCE/DOCKET NUMBER: 023070-080210US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 39:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 92 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-072-844-39
Query Match 9.4%; Score 55.5; DB 4; Length 92;
Best Local Similarity 26.0%; Pred. No. 38;
Matches 25; Conservative 2; Mismatches 28; Indels 41; Gaps 4;
QY 17 SCNAVITGA-CRRD-----VQCGAGTCCCAISLWRLGLRMTPLGRGEGEC 60
DB 6 SDFGKITGKYCBCDDFSCVRYKGMCSGHGQSCGDCDCLSDWTGYCNCNTTL-----TDTCMSNGLL 69
QY 61 HFGSHKVPFRKRKHTCPLNLLCSRFPDGRYRC 96
DB 57 -----TRTDTCMSNGLLCS-----GRGKC 76
RESULT 13
US-07-728-215-41
;/ Sequence 41, Application US/07728215
;/ Patent No. 5962643
;/ GENERAL INFORMATION:
;/ APPLICANT: Sheppard, Dean
;/ APPLICANT: Quaranta, Vito
;/ APPLICANT: Pytela, Robert
;/ TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
;/ NUMBER OF SEQUENCES: 43
;/ TITLE OF INVENTION: Thereof
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
;/ STREET: 4370 La Jolla Village Drive, Suite 700
;/ CITY: San Diego
;/ STATE: California
;/ COUNTRY: United States of America
;/ ZIP: 92122
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/07/728,215
;/ FILING DATE: 19910711
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Campbell, Cathryn A.
;/ REGISTRATION NUMBER: 31,815
;/ REFERENCE/DOCKET NUMBER: P31 8717
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (619) 535-9001
;/ TELEFAX: (619) 535-8949
;/ INFORMATION FOR SEQ ID NO: 41:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 92 amino acids
;/ TYPE: AMINO ACID
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
US-07-728-215-41
Query Match 9.3%; Score 54.5; DB 2; Length 92;
Best Local Similarity 26.8%; Pred. No. 50;
Matches 19; Conservative 1; Mismatches 26; Indels 25; Gaps 2;
QY 26 CERDVQCGAGTCCCAISLWRLGLRMTPLGRGEGECHPGSHKVPFRKRKHTCPCLPNLL 85
DB 31 CSGHGQSCGDCDCLSDWTGYCNCNTTL-----TDTCMSNGLL 69
QY 86 CSRPDPGRYRC 96
DB 70 CS-----GRGKC 76
RESULT 14
US-08-938-085A-41
;/ Sequence 41, Application US/08938085A
;/ Patent No. 6339148
;/ GENERAL INFORMATION:
;/ APPLICANT: Sheppard, Dean
;/ APPLICANT: Quaranta, Vito
;/ APPLICANT: Pytela, Robert
;/ TITLE OF INVENTION: A No. 6339148el Integrin Beta Subunit and Uses
;/ NUMBER OF SEQUENCES: 62
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, Eighth Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94111-3834
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/938,085A
;/ FILING DATE: 26-SEP-1997
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/728,215
;/ FILING DATE: 11-JUL-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Parent, Annette S.
;/ REGISTRATION NUMBER: 42,058
;/ REFERENCE/DOCKET NUMBER: 023070-080210US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 41:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 92 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
US-08-938-085A-41
Query Match 9.3%; Score 54.5; DB 4; Length 92;
Best Local Similarity 26.8%; Pred. No. 50;
Matches 19; Conservative 1; Mismatches 26; Indels 25; Gaps 2;
QY 26 CERDVQCGAGTCCCAISLWRLGLRMTPLGRGEGECHPGSHKVPFRKRKHTCPCLPNLL 85
DB 31 CSGHGQSCGDCDCLSDWTGYCNCNTTL-----TDTCMSNGLL 69
QY 86 CSRPDPGRYRC 96
DB 70 CS-----GRGKC 76
RESULT 15
US-10-072-844-41
;/ Sequence 41, Application US/10072844
;/ Patent No. 6576432
;/ GENERAL INFORMATION:
;/ APPLICANT: Sheppard, Dean
;/ APPLICANT: Quaranta, Vito

```

; Pytela, Robert
; TITLE OF INVENTION: A No. 6576432el Integrin Beta Subunit and Uses
; Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/072,844
; FILING DATE: 06-Feb-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,085A
; FILING DATE: 26-SEP-1997
; APPLICATION NUMBER: US 07/728,215
; FILING DATE: 11-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 023070-080210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
; US-10-072-844-41

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Query Match 9.3%; Score 54.5; DB 4; Length 92;
Best Local Similarity 26.8%; Pred. No. 50;
Matches 19; Conservative 1; Mismatches 26; Indels 25; Gaps 2;

QY 26 CERDVOGGAGTCCAIISLWRLGLRMCTPLGREGECHPGSHKVPFFRKRKHHTCPLNLL 85
Db 31 CSGHGQCSCDCLCDSDWTGYCNCITL-----TDCMSSNGLL 69

QY 86 CSRFDPGRYRC 96
Db 70 CS----GRGKC 76

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Search completed: January 12, 2004, 13:43:23
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:32:21 ; Search time 13 Seconds
(without alignments)
379.831 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTPDCA.....CSRPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	589	100.0	105	1 PRK1_HUMAN	P58294 homo sapien
2	310.5	52.7	81	1 VPRA_DENPO	P25687 dendroaspis
3	298	50.6	107	1 PRK2_RAT	Q84413 rattus norv
4	287.5	48.8	96	1 BV8_BOMVA	Q9PW66 bombina var
5	282.5	48.0	129	1 PRK2_HUMAN	Q9HC23 homo sapien
6	277.5	47.1	128	1 PRK2_MOUSE	Q9GXU7 mus musculu
7	107.5	18.3	224	1 DKX4_HUMAN	Q9UBT3 homo sapien
8	107.5	18.3	350	1 DKX3_CHICK	Q90839 gallus gall
9	102	17.3	259	1 DKX2_HUMAN	Q9UBU2 homo sapien
10	101	17.1	259	1 DKX2_MOUSE	Q9GYZ8 mus musculu
11	101	17.1	272	1 DKX1_MOUSE	O54908 mus musculu
12	100.5	17.1	350	1 DKX3_HUMAN	Q9UBP4 homo sapien
13	98.5	16.7	349	1 DKX3_MOUSE	Q9QUN9 mus musculu
14	97	16.5	266	1 DKX1_HUMAN	Q94907 homo sapien
15	85	14.4	107	1 COL_RABIT	P42890 oryctolagus
16	81	13.8	1964	1 NTCA_MOUSE	P31695 mus musculu
17	79.5	13.5	704	1 FB11_CHICK	Q73775 gallus gall
18	79	13.4	112	1 COL_HUMAN	P04118 homo sapien
19	78	13.2	70	1 CX2X_CONBE	Q9U3Z3 conus betul
20	77.5	13.2	473	1 FP2_MYGA	Q25464 mytilus gal
21	75	12.7	490	1 TMS2_MOUSE	Q9J1Q8 mus musculu
22	75	12.7	735	1 AD02_HUMAN	Q99965 homo sapien
23	75	12.7	1581	1 LMG3_MOUSE	Q9R0B6 mus musculu
24	75	12.7	2003	1 NTCA_HUMAN	Q99466 homo sapien
25	75	12.7	2318	1 NTCA_MOUSE	Q61982 mus musculu
26	75	12.7	2319	1 NTG3_RAT	Q9R172 rattus norv
27	74.5	12.6	113	1 COL_MOUSE	Q9CQC2 mus musculu
28	74	12.6	111	1 COL_SPECTR	Q91X17 spermophiliu
29	74	12.6	112	1 COL_RAT	P17084 rattus norv
30	73.5	12.5	2715	1 TRX2_HUMAN	Q9UMN6 homo sapien
31	73	12.4	417	1 TR16_MOUSE	Q9Z0W1 mus musculu
32	73	12.4	461	1 TRIB1_HUMAN	P20333 homo sapien
33	73	12.4	2871	1 FBN1_PIG	Q9TV36 sus scrofa

ALIGNMENTS

RESULT 1

ID	PRK1_HUMAN	STANDARD;	PRT;	105 AA.
AC	P58294;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF) (Mambakine).			
GN	PROK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21160229; PubMed=11259612;			
RA	Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.Y.;			
RT	"Identification of two prokineticin cDNAs: recombinant proteins potentially contract gastrointestinal smooth muscle.";			
RL	Mol. Pharmacol. 59:692-698(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21419730; PubMed=11528470;			
RA	Lecouter J., Kowalski J., Foster J., Hass P., Zhang Z.,			
RA	Dillard-Telm L., Frantz G., Rangell L., Deguzman L., Keller G.-A.,			
RT	Peale P., Gurney A., Hillan K.J., Ferrara N.;			
RT	"Identification of an angiogenic mitogen selective for endocrine gland endothelium.";			
RL	Nature 412:877-884(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RT	Fraser C.;			
RT	"Mambakine, a snake venom related endocrine hormone that controls macrophages.";			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle. Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary, testis, adrenal and placenta.			
CC	-!- SIMILARITY: BELONGS TO THE PROKINETICIN FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF333024; AAK49918.1; -			
DR	EMBL; AY029225; AAK33111.1; -			

DR	Genew; HGNC:18454; PROK1.
DR	MIM; 606233; -
KW	Mitogen; Growth factor; Signal.
FT	SIGNAL 1 19 BY SIMILARITY.
FT	CHAIN 20 105 PROKINETICIN 1.
FT	DISULFID 26 38 BY SIMILARITY.
FT	DISULFID 32 50 BY SIMILARITY.
FT	DISULFID 37 78 BY SIMILARITY.
FT	DISULFID 60 86 BY SIMILARITY.
FT	DISULFID 80 96 BY SIMILARITY.
SEQUENCE	105 AA; 11715 MW; C7E3FDE30EFB416A CRC64;
Query Match	100.0%; Score 589; DB 1; Length 105;
Best Local Similarity	100.0%; Pred. No. 4.9e-54;
Matches 105; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MRGATRVISMLLVTVSDCAVITGACERDVQCAGTCCCAISLWLRLMCTPLRGREGEC 60
DB	1 MRGATRVISMLLVTVSDCAVITGACERDVQCAGTCCCAISLWLRLMCTPLRGREGEC 60
QY	61 HPGSHKVPPFRKRKHHTCPCPLNLLCSRFPDGRYRCMDLNKNIF 105
DB	61 HPGSHKVPPFRKRKHHTCPCPLNLLCSRFPDGRYRCMDLNKNIF 105
RESULT 2	
VPRA_DENPO	STANDARD; PRT; 81 AA.
ID	VPRA_DENPO STANDARD; PRT; 81 AA.
AC	P25687;
DT	01-MAY-1992 (Rel. 22, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DE	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Intestinal toxin 1 (MIT 1) (MIT1) (Venom protein A).
OS	Dendroaspis polylepsis polylepis (Black mamba).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Elapidae; Elapinae; Dendroaspis.
OX	NCBI_TaxID=8620;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=Venom;
RX	MEDLINE=81115818; PubMed=7461607;
RA	Joubert F.J., Strydom D.J.;
RT	"Snake venom. The amino acid sequence of protein A from Dendroaspis
RT	polylepis polylepis (black mamba) venom.";
RL	Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
RN	[2]
RP	CHARACTERIZATION.
RC	MEDLINE=20036442; PubMed=10567694;
RA	Schweitz H., Pascaud P., Diochet S., Moinier D., Lazdunski M.;
RT	"MIT1, a black mamba toxin with a new and highly potent activity on
RT	intestinal contraction.";
RL	FEBS Lett. 461:183-188(1998).
RN	[3]
RP	STRUCTURE BY NMR.
RC	TISSUE=Venom;
RX	MEDLINE=98437381; PubMed=9761684;
RA	Boisbovier J., Albrand J.-P., Blackledge M., Jaquinod M.,
RA	Schweitz H., Lazdunski M., Marion D.;
RT	"A structural homologue of colipase in black mamba venom revealed by
RT	NMR floating disulphide bridge analysis.";
RL	J. Mol. Biol. 283:205-219(1998).
CC	-1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- SIMILARITY: BELONGS TO THE PROKINECITIN FAMILY.
DR	PDB; L1MT; 20-APR-99.
KW	Toxin; 3D-structure.
FT	DISULFID 7 19
FT	DISULFID 13 31
FT	DISULFID 18 60
FT	DISULFID 41 68
FT	DISULFID 62 78
FT	VARIANT 73 73
KW	P -> O (IN PROTEIN A').

FT	CONFLICT 18 18 C -> S (IN REF. 1).
FT	CONFLICT 22 22 S -> C (IN REF. 1).
SEQ	SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;
Query Match	52.7%; Score 310.5; DB 1; Length 81;
Best Local Similarity	62.8%; Pred. No. 1.7e-25;
Matches 49; Conservative	14; Mismatches 14; Indels 1; Gaps 1;
QY	20 AVITGACERDVQCAGTCCCAISLWLRLMCTPLRGREGECPSHKVPFRKR-K-HHHC 78
DB	1 AVITGACERDLQCGKGTCGCAVSLWKSVRVCTGVGTSGDCHPASHKIPFGSKQMHHHC 60
QY	79 PCPLNLLCSRFPDGRYRC 96
DB	61 PCAENLACVQTSPKKFKC 78
RESULT 3	
PKR2_RAT	STANDARD; PRT; 107 AA.
ID	PKR2_RAT STANDARD; PRT; 107 AA.
AC	Q8R4I3; 2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Prokineticin 2 precursor (PK2).
GN	PROK2.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Sprague-Dawley;
EX	MEDLINE=22050031; PubMed=12054613;
RA	Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibaashi Y., Suenaga M.,
RA	Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA	Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT	"Isolation and identification of EG-VEGF/prokineticins as cognate
RT	ligands for two orphan G-protein-coupled receptors.";
RL	Biochem. Biophys. Res. Commun. 293:396-402(2002).
RN	[2]
RP	EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RC	MEDLINE=2202134; PubMed=1204206;
RA	Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA	Weaver D.R., Leal F.M., Zhou Q.-Y.;
RT	"Prokineticin 2 transmits the behavioural circadian rhythm of the
RT	suprachiasmatic nucleus.";
RL	Nature 417:405-410(2002).
CC	-1- FUNCTION: May function as an output molecule from the
CC	suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC	rhythm. May also function locally within the SCN to synchronize
CC	output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC	similarity).
CC	-1- SUBUNIT: Binds to PKR1 and PKR2, both are G-protein coupled
CC	receptors.
CC	-1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC	-1- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC	lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC	-1- INDUCTION: Activated by clock and Bmal heterodimers and light;
CC	inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC	genes (CRY1 and CRY2) (Probable).
CC	-1- SIMILARITY: BELONGS TO THE PROKINECITIN FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC	the European Bioinformatics Institute. There are no restrictions on its
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CC	or send an email to license@isb-sib.ch).
CC	EMBL; AY089984; AAC09105.1; -.
DR	Neuropeptide; Biological rhythms; Signal.
KW	


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FT DISULFID 40 58 BY SIMILARITY.
FT DISULFID 45 107 BY SIMILARITY.
FT DISULFID 68 115 BY SIMILARITY.
FT DISULFID 109 125 BY SIMILARITY.
FT VARSPLIC 75 95 Missing (in isoform 2).
FT SEQUENCE 129 AA; 14314 MW; 048767958700DA55 CRC64;

Query Match 48.0%; Score 282.5; DB 1; Length 129;
Best Local Similarity 44.4%; Pred. No. 2e-22;
Matches 48; Conservative 15; Mismatches 24; Indels 21; Gaps 1;

QY 10 MLLVTVPSCAVITGACRDVCGAGTCACISLWLRGLRMCTPLRGREGCECHGSHK--- 66
DB 18 LLLTPRAGDAVITGACDKDSQCGGNCACVSIWVKSIRICTPVGKLGDSCHPLTRKNKF 77

QY 67 -----VFFFRKRKHHTCPCLNLLCSRFDPDGRYRC 96
DB 78 GNGRQERRKRKRKRKEVFFGRMRHHTCPCLGGLCLRTSFNRFTIC 125

RESULT 6
PRK2 MOUSE STANDARD; PRT; 128 AA.
AC Q9QXU7; Q9QXU6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prokineticin 2 precursor (PK2) (protein Bv8 homolog).
GN PROK2 OR Bv8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=129/SVJ;
RX MEDLINE=20047850; PubMed=10580115;
RA Wechsberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.;
RT "The mammalian homologue of Bv8 from frog skin is mainly expressed in
RT spermatocytes.";
RL FEBS Lett. 462:177-181(1999).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC STRAIN=129/SVJ;
RX MEDLINE=20510004; PubMed=11054548;
RA Jilek A., Engel E., Beier D., Lepperdinger G.;
RT "Murine Bv8 gene maps near a syntenic breakpoint of mouse chromosome 6
RL and human 3p21.";
RN [3]
RN Gene 256:189-195(2000).
RN SEQUENCE FROM N.A. (ISOFORM 2), AND FUNCTION.
RC STRAIN=C57BL/6J;
RX MEDLINE=2022134; PubMed=12024206;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Scorch K.-F.,
RA Suzuki H., Togo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (by
CC similarity).
CC -!- SUBUNIT: Binds to PKR1 and PKR2, both are G-protein coupled
CC receptors.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Bv8-a;
CC IsoId=Q9QXU7-1; Sequences=Displayed;
CC Name=2; Synonyms=Bv8-b;
CC IsoId=Q9QXU7-2; Sequences=VSP_005220;
CC Name=3;
CC IsoId=Q9QXU7-3; Sequences=VSP_005221;
CC -!- TISSUE SPECIFICITY: Expressed in the SCN and among a few other
CC discrete brain areas, including the islands of Calleja, medial
CC preoptic area of the hypothalamus and the shell of the nucleus
CC accumbens. Highly expressed in testis. In the SCN, expression
CC subjected to high amplitude of circadian oscillation.
CC -!- DEVELOPMENTAL STAGE: Expressed in mid-late pachytene spermatocytes
CC at the stages VII, VIII and IX of the semiferous epithelial cycle.
CC -!- INDUCTION: Activated by Clock and Bmal heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2).
CC -!- SIMILARITY: BELONGS TO THE PROKINETICIN FAMILY.
CC
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CC
CC -----
CC EMBL; AF182064; AAF15259.1; -
CC EMBL; AF182065; AAF15260.1; -
CC EMBL; AF182066; AAF15261.1; -
CC EMBL; AF182068; AAG09439.1; -
CC EMBL; AF182067; AAG09439.1; JOINED.
CC EMBL; AF487280; AAM49572.1; -
CC EMBL; AK015462; BAB29857.1; -
CC HSSP; P25687; 11MT.
CC MGD; MGI:1354178; Prok2.
CC Neuropeptide; Biological rhythms; Signal; Alternative splicing.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 128 PROKINETICIN 2.
FT DISULFID 33 45 BY SIMILARITY.
FT DISULFID 39 57 BY SIMILARITY.
FT DISULFID 44 106 BY SIMILARITY.
FT DISULFID 67 114 BY SIMILARITY.
FT DISULFID 108 124 BY SIMILARITY.
FT VARSPLIC 74 94 Missing (in isoform 2).
FT VARSPLIC 74 128 /FTId=VSP_005220.
FT SEQUENCE 128 AA; 14185 MW; 5F08BA177FDD858C CRC64;
FT SHVANGQRERRKRKRKRKEVFFGRMRHHTCPCLGGLAC
FT LRTSFNRFTICLARK -> VSVCTGILGVPSH (in
FT isoform 3).
FT /FTId=VSP_005221.
SQ SEQUENCE 128 AA; 14185 MW; 5F08BA177FDD858C CRC64;

Query Match 47.1%; Score 277.5; DB 1; Length 128;
Best Local Similarity 40.7%; Pred. No. 6.4e-22;
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Matches 50; Conservative 19; Mismatches 25; Indels 29; Gaps 2;
QY 3 GATRVSIMLLVTV-----SDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLG 54
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2 GPCRAPLILLLLPLLPFPAGDAVITGADKDSQCGGMCVAVIWKIRICTPVG 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 55 RGEECHPGSHK-----VPFRRKRKHTCTCLNLCSPFPDGR 93
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 QVGDSCHLPTLRKSHVANGRQERRAKRRKRKEVPWGRMRMHTCTCLPLGLACLRFSNR 121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 94 YRC 96
| |
| |
Db 122 FIC 124
| |
| |
RESULT 7
DKK4 HUMAN
ID DKK4_HUMAN STANDARD; PRT; 224 AA.
AC Q9UBT3; Q9Y4C3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dickkopf related protein-4 precursor (Dkk-4) (hdkk-4).
GN DKK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-28 AND 134-144.
RX MEDLINE=20035735; PubMed=10570958;
RA Krupnik V.B., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
RA Amatavadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,
RA Duong T., Goodearl A.D.J., Gearring D.P., Sokol S.Y., McCarthy S.A.;
RT "Functional and structural diversity of the human Dickkopf gene
RT family.";
RL Gene 238:301-313(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Tate G., Mitsuya T.;
RT "Human Dickkopf as well as DAN family members, Cerberus and Gremlin,
RT are preferentially expressed in the epithelial malignant cell lines.";
RL J. Biochem. Mol. Biol. Biophys. 3:239-242(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Tate G., Suzuki T., Mitsuya T.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CEREBELLUM, T-CELLS, ESOPHAGUS,
CC AND LUNG.
CC -!- PTM: APPEARS NOT TO BE GLYCOSYLATED.
CC -!- PTM: CAN ALSO BE PROTEOLYTICALLY PROCESSED BY A FUZIN-LIKE
CC PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC
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CC -----
CC EMBL; AF177397; AAF02677.1; -.
CC EMBL; AB018005; BAA33475.1; -.
CC EMBL; AB018003; BAA33475.1; JOINED.
CC EMBL; AB018004; BAA33475.1; JOINED.
CC EMBL; AB017788; BAA33438.1; -.
CC HSSP; P25687; 1IMT.
CC Genew; HGNC:2894; DKK4.
CC MIM; 605417; -.
CC GO; GO:0030178; P:negative regulation of Wnt receptor signal. . .; NAS.
DR InterPro; IPR006796; dickkopf_N.
DR Pfam; PF04706; dickkopf_N; 1.
KW Developmental protein; Signal; Wnt signaling pathway.
FT SIGNAL 1 18 DICKKOPF RELATED PROTEIN-4. SHORT FORM.
FT CHAIN 19 224 DICKKOPF RELATED PROTEIN-4. SHORT FORM.
FT CHAIN 134 224 DKK-TYPE CYS-1.
FT DOMAIN 41 90 DKK-TYPE CYS-2.
FT DOMAIN 145 218 M -> L (IN REF. 3).
FT CONFLICT 93 93 45F8EBC476961357 CRC64;
SQ SEQUENCE 224 AA; 24875 MW; 45F8EBC476961357 CRC64;
Query Match 18.3%; Score 107.5; DB 1; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.00033;
Matches 22; Conservative 5; Mismatches 32; Indels 3; Gaps 1;
QY 25 ACERDVQCGAGTCCCAISLWLRGLRMCTPLGRGEGECHPGSHKVPFRRKRKHTCTCLNLC 84
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 144 SCLRTFDGPGGLCCARHFW---TKICKPVLLGQVCSRRGHKDTAQAPEIFORDCGPGL 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 85 LC 86
| |
| |
Db 201 LC 202
| |
| |
RESULT 8
DKK3 CHICK
ID DKK3_CHICK STANDARD; PRT; 350 AA.
AC Q90839;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dickkopf related protein-3 precursor (Dkk-3) (Dickkopf-3) (Lens fiber
DE protein CLPESF4).
GN DKK3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Lens fibers;
RX MEDLINE=96437509; PubMed=8840185;
RA Sawada K., Agata K., Eguchi G.;
RT "Characterization of terminally differentiated cell state by
RT categorizing cDNA clones derived from chicken lens fibers.";
RL Int. J. Dev. Biol. 40:531-535(1996).
CC -!- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN EYE LENS.
CC -!- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC
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CC -----
CC EMBL; D26311; BAA05373.1; -.
CC HSSP; P25687; 1IMT.
DR InterPro; IPR006796; dickkopf_N.
DR Pfam; PF04706; dickkopf_N; 1.
KW Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 350 DICKKOPF RELATED PROTEIN-3.
FT DOMAIN 139 187 DKK-TYPE CYS-1.
FT DOMAIN 200 277 DKK-TYPE CYS-2.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 282 282 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 350 AA; 39208 MW; 57BE7ED850089DAE CRC64;

Query Match 18.3%; Score 107.5; DB 1; Length 350;
Best Local Similarity 35.8%; Pred. No. 0.0005;
Matches 24; Conservative 5; Mismatches 31; Indels 7; Gaps 2;

QY 26 CERDVCGAGTCCATSLMLRGLRMCTPLGREGECHPGSHKV-----PPFRKRKHTCP 79
DB 200 CENQHCNPGTCCAFOKELL-FPVCTPLPEEGPCHDPSNRLNLITWLEPDGVLERCP 258
QY 80 CLPNLNC 86
DB 259 CASGLIC 265

RESULT 9
DKK2 HUMAN
ID DKK2_HUMAN STANDARD; PRT; 259 AA.
AC Q9UBU2; Q9UTU3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DICKKOPF related protein-2 precursor (Dkk-2) (Dkk-2).
GN DKK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=20035735; PubMed=10570958;
RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
RA Amaravadi L., Brown D.E., Guyot D., Mays G., Leib K., Chang B.,
RA Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.;
RT "Functional and structural diversity of the human DICKKOPF gene
RL Gene 238:301-313 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Tanaka S., Sugimachi K., Sugimachi K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 75-259 FROM N.A.
RA Tate G., Suzuki T., Mitsuura T.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SKELETAL MUSCLE AND
CC LUNG.
CC -!- PTM: MAY BE PROTEOLYTICALLY PROCESSED BY A FURIN-LIKE PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
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CC
CC EMBL; AF173795; AAF02675.1; -.
CC EMBL; AB033208; BAA85465.1; -.
CC EMBL; AB035181; BAA87056.1; -.
CC EMBL; AB035180; BAA87056.1; JOINED.
CC Genew; HGNC:2892; DKK2.
CC MIM; 605415; -.
CC GO; GO:0005615; C:extracellular space; TAS.
CC InterPro; IPR006796; dickkopf_N.
CC Pfam; PF04706; dickkopf_N; 1.
CC Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
CC SIGNAL 1 33
CC POTENTIAL.
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FT CHAIN 34 259 DICKKOPF RELATED PROTEIN-2.
FT DOMAIN 78 127 DKK-TYPE CYS-1.
FT DOMAIN 183 256 DKK-TYPE CYS-2.
FT CARBOHYD 52 52 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 259 AA; 28447 MW; 39DDA3FA8975B87F CRC64;

Query Match 17.3%; Score 102; DB 1; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0014;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVCGAGTCCATSLMLRGLRMCTPLGREGECHPGSHKV-----PPFRKRKHTCPCL 81
DB 183 CLRSDSDICGFCARHFV---TKICKPVLHQEVCTKORKKSGHGLEIFQR-----CDCA 234
QY 82 PNLLCSRPPDGRY 94
DB 235 KGLSCKVWKDATY 247

RESULT 10
DKK2 MOUSE
ID DKK2_MOUSE STANDARD; PRT; 259 AA.
AC Q9QXZ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DICKKOPF related protein-2 precursor (Dkk-2) (Dkk-2).
GN DKK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99425169; PubMed=10495270;
RA Monaghan P.A., Kloschis P., Wu W., Zuniga A., Bock D., Poustka A.,
RA Delius H., Niehrs C.;
RT "Dickkopf genes are co-ordinately expressed in mesodermal lineages.";
RL Mech. Dev. 87:45-56 (1999).
CC -!- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: MAY BE PROTEOLYTICALLY PROCESSED BY A FURIN-LIKE PROTEASE.
CC -!- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC
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CC
CC EMBL; AJ243963; CAB60110.1; -.
CC MGD; MGI:1890663; DKK2.
CC InterPro; IPR006796; dickkopf_N.
CC Pfam; PF04706; dickkopf_N; 1.
CC Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
CC SIGNAL 1 33
CC POTENTIAL.
FT CHAIN 34 259 DICKKOPF RELATED PROTEIN-2.
FT DOMAIN 78 127 DKK-TYPE CYS-1.
FT DOMAIN 183 256 DKK-TYPE CYS-2.
FT CARBOHYD 52 52 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 259 AA; 28416 MW; EAA876F2D2C9780D CRC64;

Query Match 17.1%; Score 101; DB 1; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.0018;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVCGAGTCCATSLMLRGLRMCTPLGREGECHPGSHKV-----PPFRKRKHTCPCL 81
DB 183 CLRSDSDICGFCARHFV---TKICKPVLHQEVCTKORKKSGHGLEIFQR-----CDCA 234
QY 82 PNLLCSRPPDGRY 94
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DB      235 KGLSCKVWKDATY 247
| | | | |
RESULT 11
DKK1_MOUSE
ID      DKK1_MOUSE      STANDARD;      PRT;      272 AA.
AC      O54908;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Dickkopf related protein-1 precursor (Dkk-1) (mDkk-1).
GN      DKK1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98111224; PubMed=9450748;
RA      Glinka A., Wu W., Delli H., Monaghan A.P., Blumenstock C., Niehrs C.;
RT      "Dickkopf-1 is a member of a new family of secreted proteins and
RT      functions in head induction.";
RL      Nature 391:357-362(1998).
CC      -!- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF030433; AAC02426.1; -.
DR      HSP; P25687; 11MT.
DR      MGD; MGI:1329040; Dkk1.
DR      InterPro; IPR006796; dickkopf_N.
DR      Pfam; PF04706; dickkopf_N; 1.
KW      Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT      SIGNAL      1      31      POTENTIAL.
FT      CHAIN      32      272      DICKKOPF RELATED PROTEIN-1.
FT      DOMAIN      86      141      DKK-TYPE CYS-1.
FT      DOMAIN      195      269      DKK-TYPE CYS-2.
FT      CARBOHYD      262      262      N-LINKED (GLCNAC...) (POTENTIAL).
SQ      SEQUENCE      272 AA; 29268 MW; AB9FA35DFA57D3EE CRC64;
Query Match      17.1%; Score 101; DB 1; Length 272;
Best Local Similarity      33.8%; Pred. No. 0.0018;
Matches      22; Conservative      8; Mismatches      23; Indels      12; Gaps      3;
QY      26 CERDVQCGAGTCALSLWRLGRLMCTPLGREGEBC-----HPGSHKVPFPRKRKHHTCPCL 81
| | | | |
DB      195. CLRSSDCAAGLCARHFV---SKICKPLKEGVCTKHKRKGSHGLEIFQR-----CYCG 246
| | | | |
QY      82 PNLLC 86
| | |
DB      247 EGLAC 251
| | |
RESULT 12
DKK3_HUMAN
ID      DKK3_HUMAN      STANDARD;      PRT;      350 AA.
AC      Q9UBP4; Q9ULB7;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Dickkopf related protein-3 precursor (Dkk-3) (hDkk-3).
GN      DKK3 OR REIC.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20035735; PubMed=10570958;
RA      Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
RA      Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,
RA      Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.;
RT      "Functional and structural diversity of the human Dickkopf gene
RT      family.";
RL      Gene 238:301-313(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Tanaka S., Sugimachi K., Sugimachi K.;
RL      Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20119095; PubMed=10652205;
RA      Tsuji T., Miyazaki M., Sakaguchi M., Inoue Y., Namba M.;
RT      "A REIC gene shows down-regulation in human immortalized cells and
RT      human tumor-derived cell lines.";
RL      Biochem. Biophys. Res. Commun. 268:20-24(2000).
RN      [4]
RP      SEQUENCE FROM N.A.
RA      Tate G., Mitsuya T.;
RL      Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21673998; PubMed=11814687;
RA      Kobayashi K., Ouchida M., Tsuji T., Hanafusa H., Miyazaki M.,
RA      Namba M., Shimizu N., Shimizu K.;
RT      "Reduced expression of the REIC/Dkk-3 gene by promoter-
RT      hypermethylation in human tumor cells.";
RL      Gene 282:151-158(2002).
RN      [6]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -!- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN HEART, BRAIN, AND SPINAL
CC      CORD.
CC      -!- PTM: N-GLYCOSYLATED.
CC      -!- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC      -----
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CC  EMBL; AF177396; AAF02676.1; -
DR  EMBL; AB033421; BAA85488.1; -
DR  EMBL; AB034203; BAA85048.1; -
DR  EMBL; AB035182; BAA87044.2; -
DR  EMBL; AB045205; BAA87044.2; JOINED.
DR  EMBL; AB045206; BAA87044.2; JOINED.
DR  EMBL; AB045207; BAA87044.2; JOINED.
DR  EMBL; AB045208; BAA87044.2; JOINED.
DR  EMBL; AB045209; BAA87044.2; JOINED.
DR  EMBL; AB045210; BAA87044.2; JOINED.
DR  EMBL; AB057591; BAB84360.1; -
DR  EMBL; AB057804; BAB84361.1; -
DR  EMBL; BC007660; AAB07660.1; -
DR  Genew; HGNC:2893; DKK3.
DR  MIM; 605416; -
DR  GO; GO:0005615; P:extracellular space; TAS.
DR  GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
DR  InterPro; IPR006796; dickkopf_N.
DR  Pfam; PF04706; dickkopf_N_1.
KW  Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT  SIGNAL 1 16 POTENTIAL.
FT  CHAIN 17 350 DICKKOPF RELATED PROTEIN-3.
FT  DOMAIN 147 195 DKK-TYPE CYS-1.
FT  DOMAIN 208 284 DKK-TYPE CYS-2.
FT  DOMAIN 338 343 POLY-ALA.
FT  CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CONFLICT 335 335 G -> R (IN REF. 4).
SQ  SEQUENCE 350 AA; 38291 MW; 72F504122B40AFFE CRC64;

Query Match 17.1%; Score 100.5; DB 1; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.0026;
Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;

QY 26 CERDVCGAGTCCAIISLMRLGL--RMCTPLRGEGECH-PGSHKVPFFKRKH-----HT 77
DB 208 CQNRDQCPGLCCAFQ---RGLLPVCTPLPVEGELCHDPASRLDLITWEPEGALDR 264

QY 78 CPCPLNLLC 86
DB 265 CPCASGLLC 273

RESULT 13
DKK3 MOUSE STANDARD; PRT; 349 AA.
AC Q9QUN9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dkkkopf related protein-3 precursor (Dkk-3) (Dkkkopf-3) (mDkk-3).
GN DKK3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99425169; PubMed=10495270;
RA Monaghan P.A., Kioschis P., Wu W., Zuniga A., Bock D., Poustka A.,
RA Delius H., Niehrs C.;
RT "Dkkkopf genes are co-ordinately expressed in mesodermal lineages.";
RL Mech. Dev. 87:45-56(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-20035735; PubMed=10570958;
RA Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
RA Anaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,
RA Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.;
RT "Functional and structural diversity of the human Dkkkopf gene

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RT family.";
Gene 238:301-313 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasekawa T., Saico R.,
RA Saico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
RL Nature 409:685-690(2001).
CC - FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY (POTENTIAL).
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN, EYE, AND HEART.
CC - SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC -----
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CC -----
DR EMBL; AJ243964; CAB60111.1; -
DR EMBL; AF177400; AAF02680.1; -
DR EMBL; AK004853; BAB23617.1; -
DR MGD; MGI:1354952; DKK3.
DR InterPro; IPR006796; dickkopf_N.
DR Pfam; PF04706; dickkopf_N_1.
KW Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 349 DICKKOPF RELATED PROTEIN-3.
FT DOMAIN 147 195 DKK-TYPE CYS-1.
FT DOMAIN 208 284 DKK-TYPE CYS-2.
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 349 AA; 38387 MW; 564CB3C4FB2EAB88 CRC64;

Query Match 16.7%; Score 98.5; DB 1; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.0042;
Matches 26; Conservative 4; Mismatches 28; Indels 11; Gaps 4;

QY 26 CERDVCGAGTCCAIISLMRLGL--RMCTPLRGEGECH-PGSHKVPFFR-----KXKHH 77
DB 208 CQNRDQCPGLCCAFQ---RGLLPVCTPLPVEGELCHDPTSQLDLITWEPEGALDR 264

QY 78 CPCPLNLLC 86
DB 265 CPCASGLLC 273

RESULT 14
DKK1 HUMAN
ID DKK1 HUMAN
AC O94907;
PRT; 266 AA.

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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dckkpf related protein-1 precursor (Dkk-1) (Dckkpf-1) (hdkk-1)
DE (SK).
GN DKK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Leiomysarcoma;
RX MEDLINE=99315900; PubMed=10383463;
RA Fedi P., Bafio A., Nieto Soria A., Burgess W.H., Miki T.,
RA Bottaro D.P., Kraus M.H., Aaronson S.A.;
RT "Isolation and biochemical characterization of the human Dkk-1
RT homologue, a novel inhibitor of mammalian Wnt signaling.";
RL J. Biol. Chem. 274:19465-19472(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Fetal kidney;
RX MEDLINE=20035735; PubMed=10570958;
RA Krupnik V.B., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
RA Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,
RA Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.;
RT "Functional and structural diversity of the human Dkkpf gene
RT family";
RL Gene 238:301-313(1999).
RN [3]
RN SEQUENCE FROM N.A.
RA Tate G., Suzuki T., Mitsuura T.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=20422487; PubMed=10965128;
RA Roessler E., Du Y., Glinka A., Dutra A., Niehrs C., Muenke M.;
RT "The genomic structure, chromosome location, and analysis of the human
RT DKK1 head inducer gene as a candidate for holoprosencephaly.";
RN Cytogenet. Cell Genet. 89:220-224(2000).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.P., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF127563; AAD21087.1; -
CC EMBL; AF177394; AAF02674.1; -
CC EMBL; AB020315; BAA34651.1; -
CC EMBL; AB020314; BAA34651.1; JOINED.
CC EMBL; AF261158; AAG15544.1; -
CC EMBL; AF261157; AAG15544.1; JOINED.
CC EMBL; BC001539; AAH01539.1; -
CC EMBL; BC001539; AAH01539.1; -
CC MIM; 605189; -
CC GO; GO:0008083; F: growth factor activity; TAS.
CC GO; GO:0004871; F: signal transducer activity; TAS.
CC InterPro; IPR006796; dckkpf_N.
CC Pfam; PF04706; dckkpf_N; 1
KW Developmental protein; Signal; Wnt signaling pathway; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 266 DICKKOPF RELATED PROTEIN-1.
FT DOMAIN 85 138 DKK-TYPE CVS-1.
FT DOMAIN 189 263 DKK-TYPE CVS-2.
FT CARBOHYD 256 256 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 266 AA; 28671 MW; 5E878B2CCE4236BA CRC64;
Query Match 16.5%; Score 97; DB 1; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.0047;
Matches 21; Conservative 9; Mismatches 23; Indels 12; Gaps 3;
QY 26 CERDVQCGAGTCCALSLWRLGRLMCTPLGRGSEC-----HPGSHKVPFRKRRKHTCPCL 81
Db 189 CLRSSDCASGLCCARHPW---SKICKPVLKRGQVCTHRRKRGSHGLEIFQR-----CYCG 240
QY 82 PNLLC 86
Db 241 EGLSC 245
RESULT 15
COL_RABIT
ID COL_RABIT STANDARD; PRT; 107 AA.
AC P42890;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Colipase precursor.
GN CLPS.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=93345715; PubMed=8344444;
RA Colwell N.S., Aleman-Gomez J.A., Sasser T.L., Kumar V.B.;
RT "Cloning and characterization of rabbit pancreatic colipase.";
RL Int. J. Biochem. 25:885-890(1993).
CC -!- FUNCTION: Colipase is a cofactor of pancreatic lipase. It allows
CC the lipase to anchor itself to the lipid-water interface. Without
CC colipase the enzyme is washed off by bile salts, which have an
CC inhibitory effect on the lipase.
CC -!- FUNCTION: Enterostatin has a biological activity as a satiety
CC signal (By similarity).
CC -!- SUBUNIT: Forms a 1:1 stoichiometric complex with pancreatic
CC lipase.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the pancreas.
CC -!- SIMILARITY: BELONGS TO THE COLIPASE FAMILY.
CC -----
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CC EMBL; L06329; AAA02911.1; -
CC HSP; P02703; LPCN.
CC InterPro; IPR001981; Colipase.
CC Pfam; PF01114; Colipase; 1.
CC Pfam; PF02740; Colipase_C; 1.
CC PRINTS; PR00128; COLIPASE.
CC SMART; SM00023; COLIPASE; 1.
CC PROSITE; PS00121; COLIPASE; 1.
KW Lipid degradation; Digestion; Pancreas; Signal.
FT SIGNAL 1 17
FT PROPEP 18 22
FT CHAIN 23 107
FT DISULFID 34 45
FT DISULFID 40 56
FT DISULFID 44 78
FT DISULFID 66 86
FT DISULFID 80 104
SQ SEQUENCE 107 AA; 11271 MW; 825BA1AEB1422390 CRC64;

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Query Match 14.4%; Score 85; DB 1; Length 107;
 Best Local Similarity 27.5%; Pred. No. 0.033;
 Matches 30; Conservative 10; Mismatches 45; Indels 24; Gaps 5;

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QY 9 IMLLLVTSDCAVITG-----ACERDVQCGAGTCCCAISLWRLRLMCTPLGRE 56
Db 5 LVLLLVALSVAANPGPRGIVNLEGECLNSAQCKSG-CCHSSAL-SLARCAPKASE 62
QY 57 GEECHPGSHKVPFFRKXKHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
Db 63 NSECSPTIYGVYK-----CPCERGLTC-----EGDKSIVGSITNTNF 101

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Search completed: January 12, 2004, 13:33:44
 Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:32:22 ; Search time 35 Seconds
(without alignments)
774.158 Million cell updates/sec

Title: US-10-027-603-2
Perfect score: 589
Sequence: 1 MRGATRVSIMLLLVTSVDCS.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588	99.8	105	4 Q8TC69	Q8tc69 homo sapien
2	545	92.5	105	11 Q8R414	Q8r414 rattus norv
3	432	73.3	81	11 Q8K457	Q8k457 mus musculu
4	298.5	50.7	96	13 Q8JFQ0	Q8jfq0 bombina max
5	274.5	46.6	96	13 Q8JFE6	Q8jfe6 bombina max
6	273.5	46.4	96	13 Q8JFE8	Q8jfx8 bombina max
7	273.5	46.4	96	13 Q8JFY1	Q8jfy1 bombina max
8	269.5	45.8	96	13 Q8JFX9	Q8jfx9 bombina max
9	269.5	45.8	96	13 Q8JFY0	Q8jfy0 bombina max
10	266.5	45.2	96	13 Q8JFY2	Q8jfy2 bombina max
11	112	19.0	96	13 Q8UUX3	Q8uux3 gallus gall
12	108.5	18.4	221	11 Q8VEJ3	Q8vej3 mus musculu
13	104	17.7	255	13 Q8DDA4	Q8dda4 xenopus lae
14	101	17.1	259	11 Q8BFW0	Q8bfw0 mus musculu
15	100.5	17.1	171	4 Q43532	Q43532 homo sapien
16	100.5	17.1	215	4 Q8N294	Q8n294 homo sapien

17	99.5	16.9	277	11	Q9ES33	Q9es33 rattus norv
18	95.5	16.2	259	13	O57464	O57464 xenopus lae
19	94	16.0	240	13	O9PWH3	O9pwh3 brachydanio
20	90.5	15.4	425	11	Q8BU04	Q8bu04 mus musculu
21	88.5	15.0	640	10	Q96397	Q96397 chlamydomon
22	86	14.6	241	13	Q9W6D9	Q9w6d9 brachydanio
23	83	14.1	708	13	P87363	P87363 gallus gall
24	83	14.1	966	5	Q22378	Q22378 caenorhabdi
25	81.5	13.8	425	4	Q8N806	Q8n806 homo sapien
26	81.5	13.8	446	4	Q8NB03	Q8nb03 homo sapien
27	80.5	13.7	113	11	Q9D2E7	Q9d2e7 mus musculu
28	80.5	13.7	729	11	Q8BNH3	Q8bnh3 mus musculu
29	80.5	13.7	787	11	Q8K061	Q8k061 mus musculu
30	80	13.6	412	5	Q8T204	Q8t204 dictyosteli
31	79.5	13.5	446	4	Q8N1N5	Q8n1n5 homo sapien
32	79.5	13.5	704	13	O73774	O73774 gallus gall
33	79.5	13.5	814	5	Q8IQG6	Q8iqg6 drosophila
34	79	13.4	1664	5	Q9TVQ2	Q9tvq2 caenorhabdi
35	79	13.4	2447	13	O13149	O13149 fugu rubrip
36	78	13.2	1537	4	Q8WY29	Q8wy29 homo sapien
37	78	13.2	4599	4	Q9NZR2	Q9nzz2 homo sapien
38	77.5	13.2	2559	11	Q8R4U0	Q8r4u0 mus musculu
39	77	13.1	251	5	Q24774	Q24774 enchytraeus
40	76.5	13.0	1637	6	Q9XSV8	Q9xsv8 bos taurus
41	76.5	13.0	5146	6	Q8SPM4	Q8spm4 bos taurus
42	75.5	12.8	1574	11	O88281	O88281 rattus norv
43	75.5	12.8	1631	4	Q9Y6U6	Q9y6u6 homo sapien
44	75	12.7	1214	13	Q90YD2	Q90yd2 xenopus lae
45	75	12.7	2531	5	O16004	O16004 lytechinus

ALIGNMENTS

RESULT 1

Q8TC69	PRELIMINARY;	PRT;	105 AA.
ID	Q8TC69		
AC	O8TC69;		
DT	01-JUN-2002 (TremBLrel. 21, Created)		
DT	01-JUN-2002 (TremBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TremBLrel. 21, Last annotation update)		
DE	Prokineticin 1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RA	Strausberg R.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC025399; AAH25399.1; ..		
SQ	SEQUENCE 105 AA; 11729 MW; ES70FDE30EFBS2D2 CRC64;		

Query Match 99.8%; Score 588; DB 4; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.6e-65;
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRGATRVSIMLLLVTSVDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCCTPLGREGBEC	60
DB	1	MRGATRVSIMLLLVTSVDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCCTPLGREGBEC	60
QY	61	HPGSHKVPFFRRKHHTCPCLPNLLCSRFPPDGRYRCMDLKNINF	105
DB	61	HPGSHKVPFFRRKHHTCPCLPNLLCSRFPPDGRYRCMDLKNINF	105

RESULT 2

Q8R414	PRELIMINARY;	PRT;	105 AA.
ID	Q8R414		
AC	Q8R414;		
DT	01-JUN-2002 (TremBLrel. 21, Created)		
DT	01-JUN-2002 (TremBLrel. 21, Last sequence update)		

```
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Prokineticin 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;
RC Masuda Y., Takatsu Y., Ohtaki T.;
RA "Purification and identification of EG-VEGF family as cognate ligands
RT for two orphan G protein-coupled receptors.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY089983; AAM09104.1; -.
SQ SEQUENCE 105 AA; 11642 MW; 8DF0C42122B1C5B6 CRC64;

Query Match          92.5%; Score 545; DB 11; Length 105;
Best Local Similarity 89.5%; Pred. No. 1.2e-59;
Matches 94; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGEGEC 60
DB 1 MGRGVQVFMILLATVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGEGEC 60
QY 61 HPGSHKVPFFRKRRKHTCPCLPNLCSRPDPGRYCSMDLKNINF 105
DB 61 HPGSHKVPFFRKRRKHTCPCLPNLCSRPDPGRYCSMDLKNVNF 105

RESULT 3
Q8K457 PRELIMINARY; PRT; 81 AA.
AC Q8K457;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Prokineticin 1 (Fragment).
GN PROK1 OR PK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6;
RC MEDLINE=22022134; PubMed=12024206;
RX Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RL suprachiasmatic nucleus";
RL Nature 417:405-410(2002).
DR EMBL; AF487281; AAM49573.1; -.
DR MGD; MGI:2180370; Prok1.
FT NON TER
FT SEQUENCE 81 AA; 9192 MW; 7BBE38C6B16A8011 CRC64;

Query Match          73.3%; Score 432; DB 11; Length 81;
Best Local Similarity 87.7%; Pred. No. 8.8e-46;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 25 ACERDVQCGAGTCCCAISLWLRGLRMTPLRGEGECHPGSHKVPFFRKRRKHTCPCLPNL 84
DB 1 ACERDLCQAGTCCCAISLWLRGLRMTPLRGEGECHPGSHKVPFFRKRRKHTCPCLPNL 84

QY 85 LCSRFPDGRYCSMDLKNINF 105
DB 61 LCSRFPDGRYCSMDLKNVNF 105

RESULT 4
Q8JF00 PRELIMINARY; PRT; 96 AA.
ID Q8JF00;
AC Q8JF00;
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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Bv8 protein homolog 2.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin secretion;
RA Lai R., Liu H., Lee W.-H., Zhang Y.;
RT "Characterization and cloning of Bv8 protein homologs from toad
RT Bombina maxima.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411091; AAN03822.1; -.
SQ SEQUENCE 96 AA; 10198 MW; EC4EAA5EFE49B2F0 CRC64;

Query Match          50.7%; Score 298.5; DB 13; Length 96;
Best Local Similarity 53.6%; Pred. No. 3.4e-29;
Matches 52; Conservative 16; Mismatches 28; Indels 1; Gaps 1;

QY 1 MGRATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGEGEC 60
DB 1 MKCFAQIVVLLLVIAFSGAVITGACDRDVQCGSGTGCCAAASLWSNRNIRFCVPLGNNGEC 60
QY 61 HPGSHKVPFFRKRRKHTCPCLPNLCSRPDPGRYCS 97
DB 61 HPASHKVPYNGKRLSSLCPSCKSLTCSKSGE-KFOCS 96

RESULT 5
Q8JFE6 PRELIMINARY; PRT; 96 AA.
ID Q8JFE6;
AC Q8JFE6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Bv8-a protein precursor (Bv8 protein homolog 1).
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin;
RA Chen T., Bjourson A.J., Shaw C.;
RT "Multiple Bv8 isoforms from the skin of the Oriental toad, Bombina
RT maxima.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin secretion;
RA Lai R., Liu H., Lee W.-H., Zhang Y.;
RT "Characterization and cloning of Bv8 protein homologs from toad
RT Bombina maxima.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ440230; CAD29340.1; -.
DR EMBL; AF411090; AAN03821.1; -.
KW Signal.
FT SIGNAL
FT CHAIN
FT SEQUENCE 96 AA; 10117 MW; 2269AAC8654B18A6 CRC64;

Query Match          46.6%; Score 274.5; DB 13; Length 96;
Best Local Similarity 49.5%; Pred. No. 3.2e-26;
Matches 48; Conservative 17; Mismatches 31; Indels 1; Gaps 1;

QY 1 MGRATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGEGEC 60
DB 1 MKCFAQIVVLLLVIAFSGAVITGACDRDVQCGSGTGCCAAASLWSNRNIRFCVPLGNNGEC 60
QY 61 HPGSHKVPFFRKRRKHTCPCLPNLCSRPDPGRYCS 97
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[illegible]

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QY 1 MGRATRVSTMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBC 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 1 MKCFAIVLLVIAFAGSHAVITGVCDRAQCGSGTCCAASAFSRNIRFCVPLGNNGEBC 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 61 HPGSHKVPFRKRKHHKHTCPLNLLCSRFPPDGRYRCS 97
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 61 HPASHKVPYNGKRLSLCPCNTGLTCKSGE-KSQCS 96
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 10
Q8JFY2 PRELIMINARY; PRT; 96 AA.
AC Q8JFY2
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE BM8-b protein precursor.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Bjorson A.J., Shaw C.;
RT "Multiple BM8 isoforms from the skin of the Oriental toad, Bombina
RT maxima.";
RL EMBL; AJ440231; CAD29341.1; -.
KW SIGNAL.
FT CHAIN
FT SIGNAL
SQ SEQUENCE 96 AA; 10186 MW; D77CAACFF54B020C CRC64;

Query Match 45.2%; Score 266.5; DB 13; Length 96;
Best Local Similarity 49.5%; Pred. No. 3.1e-25;
Matches 48; Conservative 16; Mismatches 32; Indels 1; Gaps 1;

QY 1 MGRATRVSTMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBC 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 1 MKCFAIVLLVIAFAGSHAVITGVCDRAQCGSGTCCAASAFSRNIRFCVPLGNNGEBC 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 61 HPGSHKVPFRKRKHHKHTCPLNLLCSRFPPDGRYRCS 97
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 61 HPASHKVPYNGKRLSLCPCNTGLTCKSGE-KYQCS 96
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 11
Q8UUX3 PRELIMINARY; PRT; 96 AA.
AC Q8UUX3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dkk-1 (Fragment).
GN DKK-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21559221; PubMed=11702953;
RA Mukhopadhyay M., Shtrom S., Rodriguez-Esteban C., Chen L., Tsukui T.,
RA Gomer L., Dorward D.W., Glinka A., Grinberg A., Huang S.P., Niehrs C.,
RA Belmonte J.C.I., Westphal H.;
RT "Dkkopfl is required for embryonic head induction and limb
RT morphogenesis in the mouse.";
RL Dev. Cell 1:423-434 (2001).
DR EMBL; AY049017; AAL07515.1; -.
FT NON_TER 1
```

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SQ SEQUENCE 96 AA; 10756 MW; 043E6A647D5AF4E7 CRC64;

Query Match 19.0%; Score 112; DB 13; Length 96;
Best Local Similarity 33.8%; Pred. No. 4e-06;
Matches 22; Conservative 9; Mismatches 22; Indels 12; Gaps 3;

QY 26 CERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBC-----HPGSHKVPFRKRKHHKHTCPL 81
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 20 CLRSSDCAAGLCCARHF--SKICKPVLREQVCTRRHRKGAHGLEIFOR-----CPCA 71
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 82 PNLLC 86
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 72 EGMAC 76
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 12
Q8VEJ3 PRELIMINARY; PRT; 221 AA.
AC Q8VEJ3
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 23, Last annotation update)
DE Similar to dickkopf (Xenopus laevis) homolog 4.
GN DKK4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; RC018400; AAH18400.1; -.
DR MGD; MGI:2385299; DKK4.
SQ SEQUENCE 221 AA; 24260 MW; 670AD9F750BF1715 CRC64;

Query Match 18.4%; Score 108.5; DB 11; Length 221;
Best Local Similarity 35.5%; Pred. No. 2.4e-05;
Matches 22; Conservative 5; Mismatches 32; Indels 3; Gaps 1;

QY 25 ACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEBCHPGSHKVPFRKRKHHKHTCPLN 84
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 144 SCLRTSDCGPLGCCARHF--TKICKPVLREQVCSRGRHKDTAQAPEIFORCDGPG 200
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 85 LC 86
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 201 TC 202
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 13
Q9DDA4 PRELIMINARY; PRT; 255 AA.
AC Q9DDA4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Dickkopf2 precursor.
GN DKK2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu W., Glinka A., Delius H., Niehrs C.;
RT "Mutual antagonism between dickkopf1 and -2 regulates Wnt/beta-catenin
RT signalling.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ300197; CAC17815.1; -.
DR HSSP; P25687; LIMIT.
DR InterPro; IPR006796; dickkopf_N.
DR Pfam; PF04706; dickkopf_N; 1.
```

```
KW Signal.
FT CHAIN 1 29 POTENTIAL.
FT CHAIN 30 255 DICKKOPF2.
SQ SEQUENCE 255 AA; 28096 MW; F270B7DD0F4FCD73 CRC64;

Query Match 17.1%; Score 104; DB 13; Length 255;
Best Local Similarity 31.5%; Pred. No. 9.9e-05;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVQCGAGTCCATSLWLRLGRLMCTPLGREGECC-----HPGSHKVPFPRKXKHTCPCL 81
Db 179 CLRSTDCIEGFCARHFW---TKICKPVLHQEVCTKLRKKGSHGLEIFQR-----CDCA 230

QY 82 PNLLCSRFPDGRY 94
Db 231 KGLSCKVWKDATY 243

RESULT 14
Q8BFWO PRELIMINARY; PRT; 259 AA.
ID Q8BFWO
AC Q8BFWO;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE DICKKOPF related protein-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Body, and Head;
EX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK028225; BAC25824.1; -.
DR EMBL; AK031749; BAC27536.1; -.
SQ SEQUENCE 259 AA; 28432 MW; E649ED9E38C7B8E4 CRC64;

Query Match 17.1%; Score 101; DB 11; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.00024;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVQCGAGTCCATSLWLRLGRLMCTPLGREGECC-----HPGSHKVPFPRKXKHTCPCL 81
Db 183 CLRSSDCIDGFCARHFW---TKICKPVLHQEVCTKQRKKGSHGLEIFQR-----CDCA 234

QY 82 PNLLCSRFPDGRY 94
Db 235 KGLSCKVWKDATY 247

RESULT 15
O43532 PRELIMINARY; PRT; 171 AA.
ID O43532
AC O43532;
DT 01-JUN-1998 (TremBLrel. 06, Created)
DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE RIG-like 7-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Ligon A.H., Pershouse M.A., Jasser S., Hong Y.K., Yung W.K.A.,
RA Steck P.A.;
```

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RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034208; AAB92664.1; -.
DR InterPro; IPR006796; dickkopf_N.
DR InterPro; IPR005805; Rieseke.
DR Pfam; PF04706; dickkopf_N; 1.
DR PROSITE; PS00200; RIESEK_2; 1.
SQ SEQUENCE 171 AA; 19283 MW; B90E38F873D0E62 CRC64;

Query Match 17.1%; Score 100.5; DB 4; Length 171;
Best Local Similarity 37.7%; Pred. No. 0.00018;
Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;

QY 26 CERDVQCGAGTCCATSLWLRLGRLMCTPLGREGECC-----HPGSHKVPFPRKXKHTCPCL 81
Db 52 CDNRDCCQGLCCAFQ---RGLLPVCTPLPVEGELCHDPASRLDLITWELEPDGALDR 108

QY 78 CPCLFNILC 86
Db 109 CFCXSGLLC 117
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Search completed: January 12, 2004, 13:34:33
Job time : 37 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:38:53 ; Search time 34 Seconds
(without alignments)
796.927 Million cell updates/sec

Title: US-10-027-603-2
Perfect score: 589
Sequence: 1 MRGATRVSIMLLLVTSVSDCA.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 158351

Minimum DB seq length: 0

Maximum DB seq length: 105

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588	99.8	105	4 Q8TC69	Q8TC69 homo sapien
2	545	92.5	105	11 Q8R414	Q8R414 rattus norv
3	432	73.3	81	11 Q8K457	Q8K457 mus musculus
4	298.5	50.7	96	13 Q8JFQ0	Q8JFQ0 bombina max
5	274.5	46.6	96	13 Q8JFE6	Q8JFE6 bombina max
6	273.5	46.4	96	13 Q8JFX8	Q8JFX8 bombina max
7	273.5	46.4	96	13 Q8JFY1	Q8JFY1 bombina max
8	269.5	45.8	96	13 Q8JFY0	Q8JFY0 bombina max
9	269.5	45.8	96	13 Q8JFY0	Q8JFY0 bombina max
10	266.5	45.2	96	13 Q8JFY2	Q8JFY2 bombina max
11	112	19.0	96	13 Q8JUX3	Q8JUX3 gallus gall
12	72	12.2	101	10 Q85313	Q85313 lavatera th
13	66.5	11.3	98	4 Q8BYR6	Q8BYR6 homo sapien
14	65.5	11.1	99	11 Q9CPW1	Q9CPW1 mus musculus
15	65.5	11.1	99	11 Q9D7P0	Q9D7P0 mus musculus
16	65	11.0	78	10 Q9MB66	Q9MB66 nicotiana t

17	65	11.0	95	16 Q9RJN7	Q9RJN7 streptomyce
18	64.5	11.0	98	4 Q8BYR7	Q8BYR7 homo sapien
19	62	10.5	101	10 Q9XGJ3	Q9XGJ3 gerbera hyb
20	62	10.5	102	10 Q24040	Q24040 lavatera th
21	61.5	10.4	83	5 Q9XXT6	Q9XXT6 caenorhabdi
22	61	10.4	93	10 Q94HA1	Q94HA1 oryza sativ
23	61	10.4	95	2 Q9ZGV4	Q9ZGV4 escherichia
24	60.5	10.3	92	10 Q8GX79	Q8GX79 arabidopsis
25	60.5	10.3	96	16 Q9CJ11	Q9CJ11 lactococcus
26	60.5	10.3	99	11 Q9D638	Q9D638 mus musculus
27	60	10.2	84	5 Q8MN28	Q8MN28 schistosoma
28	59.5	10.1	75	10 F82734	F82734 arabidopsis
29	59.5	10.1	102	11 Q8C7K0	Q8C7K0 mus musculus
30	59	10.0	96	10 Q9N199	Q9N199 chlamydomon
31	59	10.0	99	11 Q9D248	Q9D248 mus musculus
32	59	10.0	103	10 Q9SYR2	Q9SYR2 urtica dioi
33	58	9.8	73	12 Q39545	Q39545 hepatitis g
34	58	9.8	73	12 Q39558	Q39558 hepatitis g
35	58	9.8	92	5 Q46162	Q46162 schistocerc
36	57	9.8	103	10 Q24090	Q24090 medicago tr
37	57.5	9.8	104	10 Q93X17	Q93X17 solanum tub
38	57	9.7	73	10 Q9FCG1	Q9FCG1 phaseolus a
39	57	9.7	73	12 Q39595	Q39595 hepatitis g
40	57	9.7	73	12 Q39596	Q39596 hepatitis g
41	57	9.7	73	12 Q39591	Q39591 hepatitis g
42	57	9.7	98	16 Q9RUD3	Q9RUD3 deinococcus
43	56.5	9.6	73	12 Q39594	Q39594 hepatitis g
44	56.5	9.6	78	5 Q9BP87	Q9BP87 conus arena
45	56.5	9.6	82	5 Q95QW8	Q95QW8 caenorhabdi

ALIGNMENTS

RESULT 1

Q8TC69 PRELIMINARY; PRT; 105 AA.
ID Q8TC69;
AC Q8TC69;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)
DE Prokinecin 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC025399; AAH25399.1; --
SQ SEQUENCE 105 AA; 11729 MW; E570FDE30EFB52D2 CRC64;

Query Match 99.8%; Score 588; DB 4; Length 105;
Best Local Similarity 99.0%; Pred. No. 5.6e-65;
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTSVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCPTPLGREGRC 60
Db 1 MRGATRVSIMLLLVTSVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCPTPLGREGRC 60
QY 61 HPGSHKVPFFRRKHHTCPCLPNLLCSFFPDGRYRCMDLKNINF 105
Db 61 HPGSHKVPFFRRKHHTCPCLPNLLCSFFPDGRYRCMDLKNINF 105

RESULT 2

Q8R414 PRELIMINARY; PRT; 105 AA.
ID Q8R414
AC Q8R414;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)

```
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Prokineticin 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Masuda Y., Takatsu Y., Ohtaki T.;
RT "Purification and identification of EG-VEGF family as cognate ligands
RT for two orphan G protein-coupled receptors.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AV089983; AM09104.1; -.
SQ SEQUENCE 105 AA; 11642 MW; 8DF0C42122B1C5B6 CRC64;

Query Match 92.5%; Score 545; DB 11; Length 105;
Best Local Similarity 89.5%; Pred. No. 1.2e-59;
Matches 94; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGSC 60
DB 1 MRGAVQVFMILLATVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGSC 60
QY 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPPDGRYCSMDLKNINF 105
DB 61 HPGSHKIPFFRKQKHHTCPCLPNLLCSRPPDGRYCSMDLKNVNF 105

RESULT 3
Q8K457 PRELIMINARY; PRT; 81 AA.
ID Q8K457
AC Q8K457;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Prokineticin 1 (Fragment).
GN PROK1 OR PK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=22022134; PubMed=12024206;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
DR EMBL: AF487281; AA049573.1; -.
DR MGD; MGI:2180370; Prok1.
FT NON TER 1
FT SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;

Query Match 73.3%; Score 432; DB 11; Length 81;
Best Local Similarity 87.7%; Pred. No. 8.8e-46;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 25 ACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGSCPGSHKVPFFRKHKHTCPCLPNL 84
DB 1 ACERDTCQCGAGTCCCAISLWRLGRLMCTPLRGREGSCPGSHKIPFLRKQHTCPSPSL 60

QY 85 LCSRFDPGRYCSMDLKNINF 105
DB 61 LCSRFDPGRYCSMDLKNVNF 105

RESULT 4
Q8JFQ0 PRELIMINARY; PRT; 96 AA.
ID Q8JFQ0
AC Q8JFQ0;
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DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Bv8 protein homolog 2.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]_TaxID=161274;
RP SEQUENCE FROM N.A.
RC TISSUE=Skin secretion;
RA Lai R., Liu H., Lee W.-H., Zhang Y.;
RT "Characterization and cloning of Bv8 protein homologs from toad
RT Bombina maxima.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF411091; AA03822.1; -.
SQ SEQUENCE 96 AA; 10198 MW; EC4EAA5EFE49B2F0 CRC64;

Query Match 50.7%; Score 298.5; DB 13; Length 96;
Best Local Similarity 53.6%; Pred. No. 3.4e-29;
Matches 52; Conservative 16; Mismatches 28; Indels 1; Gaps 1;

QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGSC 60
DB 1 MKCFAQIVVLLVIAFSGHAVITGACDRDVQCGSGTCCCAASLWSRNFRCVPLGNNGESC 60
QY 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPPDGRYCS 97
DB 61 HPASHKVPYNGKRLSLCPCKSGLTCSKSGE-KFOCS 96

RESULT 5
Q8JFE6 PRELIMINARY; PRT; 96 AA.
ID Q8JFE6
AC Q8JFE6;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Bv8-a protein precursor (Bv8 protein homolog 1).
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]_TaxID=161274;
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Bjournson A.J., Shaw C.;
RT "Multiple Bv8 isoforms from the skin of the Oriental toad, Bombina
RT maxima.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin secretion;
RA Lai R., Liu H., Lee W.-H., Zhang Y.;
RT "Characterization and cloning of Bv8 protein homologs from toad
RT Bombina maxima.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ40230; CAD29340.1; -.
DR EMBL; AF411090; AA03821.1; -.
KW Signal.
FT CHAIN 1 19
FT SIGNAL 20 96
FT SEQUENCE 96 AA; 10117 MW; 2269AAC8654B18A6 CRC64;

Query Match 46.6%; Score 274.5; DB 13; Length 96;
Best Local Similarity 49.5%; Pred. No. 3.2e-26;
Matches 48; Conservative 17; Mismatches 31; Indels 1; Gaps 1;

QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGSC 60
DB 1 MKCFAQIVVLLVIAFSGHAVITGACDRDVQCGSGTCCCAASLWSRNFRCVPLGNNGESC 60
QY 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPPDGRYCS 97
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QY 1 MRCATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCTCAISLWLRGLRMTPLRGREGEC 60
Db 1 MKCFAQIVVLLVIAFSGAVITGVCDRAQCGSGTCCAAAFSRNIRFCVPLGNNGEBC 60
QY 61 HPGSHKVPFRKPKHHTCPLNLLCSRPDPGRYCS 97
Db 61 HPASHKVPYNGKRLSSLCPCNTGLTCKSGE-KSQCS 96

RESULT 10
Q8JFY2 PRELIMINARY; PRT; 96 AA.
AC Q8JFY2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE BMB-b protein precursor.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Bourson A.J., Shaw C.;
RT "Multiple BMB isoforms from the skin of the Oriental toad, Bombina
maxima.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ40231; CAD29341.1; -.
KW SIGNAL.
FT CHAIN 1 19 BMB-B PROTEIN.
FT CHAIN 20 96 BMB-B PROTEIN.
SQ SEQUENCE 96 AA; 10186 MW; D77CAACFF54B020C CRC64;

Query Match 45.2%; Score 266.5; DB 13; Length 96;
Best Local Similarity 49.5%; Pred. No. 3.1e-25;
Matches 48; Conservative 16; Mismatches 32; Indels 1; Gaps 1;

QY 1 MRCATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCTCAISLWLRGLRMTPLRGREGEC 60
Db 1 MKCFAQIVVLLVIAFSGAVITGVCDRAQCGSGTCCAAAFSRNIRFCVPLGNNGEBC 60
QY 61 HPGSHKVPFRKPKHHTCPLNLLCSRPDPGRYCS 97
Db 61 HPASHKVPYNGKRLSSLCPCNTGLTCKSGE-KYQCS 96

RESULT 11
Q8UUX3 PRELIMINARY; PRT; 96 AA.
AC Q8UUX3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dkk-1 (Fragment).
GN DKK-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2155221; PubMed=11702953;
RA Mukhopadhyay M., Shtrom S., Rodriguez-Esteban C., Chen L., Tsukui T.,
RA Gomer L., Dorward D.W., Hlinka A., Grinberg A., Huang S.P., Niehrs C.,
RA Belmonte J.C.I., Westphal H.;
RT "Dkkopfl is required for embryonic head induction and limb
morphogenesis in the mouse.";
RL Dev. Cell 1:423-434(2001).
DR EMBL; AY049017; AAL07515.1; -.
FT NON_TER 1 1
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SQ SEQUENCE 96 AA; 10756 MW; 043E6A647D5AF4E7 CRC64;

Query Match 19.0%; Score 112; DB 13; Length 96;
Best Local Similarity 33.8%; Pred. No. 4e-06;
Matches 22; Conservative 9; Mismatches 22; Indels 12; Gaps 3;

QY 26 CERDVQCGAGTCCTCAISLWLRGLRMTPLRGREGEC-----HPGSHKVPFRKPKHHTCPL 81
Db 20 CLRSSDCAAGLCCARHFV---SKICKPVLREQVCTHRRKGAHGLEIFQR-----CPCA 71

QY 82 PNLLC 86
Db 72 EGMAC 76

RESULT 12
Q85313 PRELIMINARY; PRT; 101 AA.
AC Q85313;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cold-regulated LTCOR12.
GN LTCOR12.
OS Lavatera thuringiaca.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosida II; Malvales; Malvaceae; Malvoideae; Lavatera.
OX NCBI_TaxID=61660;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaves without petiole;
RA Vazquez-Tello A.;
RT "Cloning and characterization of low temperature-regulated genes from
Lavatera thuringiaca.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF060569; AAC15460.1; -.
DR InterPro; IPR003854; GASA.
DR Pfam; PF02704; GASA; 1.
SQ SEQUENCE 101 AA; 10549 MW; D303D53E17E2D111 CRC64;

Query Match 12.2%; Score 72; DB 10; Length 101;
Best Local Similarity 19.3%; Pred. No. 0.38;
Matches 22; Conservative 16; Mismatches 26; Indels 50; Gaps 5;

QY 7 VSIMLLTVTSCAVITGACE-----RDVQCG-----AGTCCAISL 42
Db 13 ISLLIIQIVEADHQLVTSASGSPFKIDCGGACAAACQLSSRPHLCRACGTCCARS- 71
QY 43 WLRLGLRMTPLRGREGECHPGSHKVPFRKPKHHTCPLNLLCSRPDPGRYRC 96
Db 72 -----RCVPPGTAGNQ-----EMCPCVSLTTH---GGRKRC 100

RESULT 13
Q9BYR6 PRELIMINARY; PRT; 98 AA.
AC Q9BYR6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Keratin associated protein 3.3.
GN KRTAP3.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Scalp;
RA Rogers M.A.; Langbein L., Winter H., Ehmann C., Korn B., Schweizer J.;
RT "Characterization of a cluster of human high/ ultrahigh keratin
associated proteins on chromosome 17q12-21.";
```


RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ406933; CAC27572.1; --
DR Genew; HGNC:18890; KRTAP3-3.

SQ SEQUENCE 98 AA; 10365 MW; 9807DC59B72799AB CRC64;

Query Match 11.3%; Score 66.5; DB 4; Length 98;

Best Local Similarity 27.9%; Pred. No. 1.8; Indels 25; Gaps 5;
Matches 20; Conservative 6; Mismatches 21; Indels 29; Gaps 6;

QY 19 CAVITG----ACERDVQCGAGTC----CAISLWRLGLRMCTPLGREGECHPGSHKVPFF 70

Db 9 CSVPTGPATTCSSDKSCRCGVLPSCTCPHTVWLEPTCC-----DNCPPCH-IP-- 58

QY 71 RKRKHHTCPCPLP 82

Db 59 -----QPCVP 63

RESULT 14

Q9CPW1

ID Q9CPW1 PRELIMINARY; PRT; 99 AA.

AC Q9CPW1

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE 2310020D06RIK protein (473340116RIK protein).

GN 2310020D06RIK OR 473340116RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Tongue; and Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK010142; BAB26727.1; --

DR EMBL; AK003615; BAB22891.1; --

DR EMBL; AK009410; BAB26270.1; --

DR MGD; MGI:1913630; 2310020D06RIK.

DR MGD; MGI:1913958; 473340116RIK.

SQ SEQUENCE 99 AA; 10574 MW; F0E5542FA890302B CRC64;

Query Match

Best Local Similarity 11.1%; Score 65.5; DB 11; Length 99;

Matches 22; Conservative 6; Mismatches 28; Indels 29; Gaps 6;

QY 19 CAVITG----ACERDVQCGAGTC----CAISLWRLGLRMCTPLGREGECHPGSHKVPFF 70

Db 9 CSVPTGPATTCSSDKSCRCGVLPSCTCPHTVWLEPTCC-----DNCPPCH-IP-- 58

QY 71 RKRKHHTCPCPLNLL-----CSRFPD 91

Db 59 -----QPCVPTCFLNSCHPTPD 76

RESULT 15

Q9D7P0

ID Q9D7P0 PRELIMINARY; PRT; 99 AA.

AC Q9D7P0

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE 2310020D06RIK protein.

GN 2310020D06RIK

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Tongue;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK009052; BAB26048.1; --

DR MGD; MGI:1913630; 2310020D06RIK.

SQ SEQUENCE 99 AA; 10531 MW; 61D7550FB76E2FCA CRC64;

Query Match

Best Local Similarity 11.1%; Score 65.5; DB 11; Length 99;

Matches 22; Conservative 6; Mismatches 28; Indels 29; Gaps 6;

QY 19 CAVITG----ACERDVQCGAGTC----CAISLWRLGLRMCTPLGREGECHPGSHKVPFF 70

Db 9 CSVPTGPATTCSSDKSCRCGVLPSCTCPHTVWLEPTCC-----DNCPPCH-IP-- 58

QY 71 RKRKHHTCPCPLNLL-----CSRFPD 91

Db 59 -----QPCVPTCFLNSCHPTPD 76

Search completed: January 12, 2004, 13:42:16

Job time : 35 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:32:22 ; Search time 21 Seconds
(without alignments)
480.843 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTSQCA.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	100.5	17.1	350	JC7188	REIC protein - hum
2	88.5	15.0	640	T08179	LRGS protein - Chl
3	83	14.1	1101	T16840	hypothetical prote
4	81	13.8	1964	T09059	notch4 - mouse
5	79	13.4	112	XLHU	colipase precursor
6	77.5	13.2	473	A56175	adhesive plaque pr
7	77	13.1	251	A55035	cysteine-rich prot
8	75.5	12.8	1574	T13954	MEGF6 protein - ra
9	75	12.7	734	JC4861	fertilin beta cha
10	75	12.7	2318	S45306	notch 3 protein -
11	75	12.7	2531	T31070	notch homolog - ae
12	74	12.6	112	I51909	colipase precursor
13	74	12.6	1620	T27283	hypothetical prote
14	73	12.4	461	A35156	tumor necrosis fac
15	73	12.4	3075	S14458	laminin alpha-1 ch
16	72.5	12.3	643	T25473	hypothetical prote
17	72.5	12.3	2871	A55567	fibrillin I - bovi
18	72.5	12.3	3002	A47221	fibrillin I precu
19	72	12.2	1639	MF5FB2	laminin gamma-1 ch
20	71.5	12.1	591	I48141	acroganin - guine
21	71.5	12.1	601	B36346	fibulin 1 precursor
22	71.5	12.1	683	C36346	fibulin 1 precursor
23	71.5	12.1	1178	A33804	thrombospondin pre
24	71.5	12.1	1854	T13576	hypothetical prote
25	71	12.1	286	S34665	collagen, cuticula
26	71	12.1	593	GYHU	granulin precursor
27	70.5	12.0	1847	T18308	probable vitellogen
28	70.5	12.0	2871	A55624	fibrillin-1 precu
29	69.5	11.8	802	T24293	hypothetical prote

ALIGNMENTS

RESULT 1

JC7188

REIC protein - human

C:Species: Homo sapiens (man)

C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

C:Accession: JC7188

R:Taugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.

Biochem. Biophys. Res. Commun. 268, 20-24, 2000

A:Title: A REIC gene shows down-regulation in human immortalized cells and human tumor-

A:Reference number: JC7188; MUID:20119095; PMID:10652205

A:Accession: JC7188

A:Molecule type: mRNA

A:Residues: 1-350 <TSU>

A:Cross-references: DBBJ:AB034203

A:Experimental source: heart

C:Comment: This protein is a secreted glycoprotein for head induction in amphibian embryo

C:Genetics:

A:Gene: reic

C:Superfamily: human REIC protein

C:Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor

Query Match

Best Local Similarity

Matches 26; Conservative

26; Indels 11; Gaps 4;

26 CERVQCCAGTCCALSLWRLGL--RMCTPLGREGEC-PGSHKVPFPRKRKH-----HT 77

208 CDNRDCQCPGLCCAFQ---RGLLPVCTPLPVEGELCHDPASRLDLITWELEPDGALDR 264

78 CPCLPNLILC 86

265 CPCASGLLIC 273

RESULT 2

T08179

LRGS protein - Chlamydomonas reinhardtii

C:Species: Chlamydomonas reinhardtii

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999

C:Accession: T08179

R:Gloeckner, G.; Beck, C.F.

submitted to the EMBL Data Library, October 1996

A:Description: Molecular characterization of a gene (LRGS) involved in blue light signal

A:Reference number: Z16399

A:Accession: T08179

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-640 <GLO>

A:Cross-references: EMBL:U73817; NID:gl644369; PID:gl644370

C:Genetics:

A:Gene: LRGS

Query Match 15.0%; Score 88.5; DB 2; Length 640;
Best Local Similarity 31.6%; Pred. No. 0.24; 24; Indels 23; Gaps 4;
Matches 24; Conservative 5; Mismatches 23; Indels 23; Gaps 4;
QY 32 CGAGTCCCAISLWRLGRLMCTPLGRGEECHPGSHKVPFFRKRKHTCPLCNLLCSRF-- 89
DB 488 CTAGGCC---NM---TCLPMWGSGLTWPRLMTP-----SRTACCLPTPCSSRWLR 533
QY 90 -----PDGRYRCSM 98
DB 534 RWRGMAPGGRWRCSL 549
RESULT 3
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16840
R:Geisels, C.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1101 <GEI>
A:Cross-references: EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1; CESP:T10E10
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match 14.1%; Score 83; DB 2; Length 1101;
Best Local Similarity 24.4%; Pred. No. 1.4;
Matches 32; Conservative 9; Mismatches 40; Indels 50; Gaps 6;
QY 13 LVTVSDCAVITGNCERDVCGAGTCCCAISLWRLG-----SHKVPFFRKRKHTCPLCNLLCS 46
DB 749 LMSVQRCAWIG-CPPGNOCENGVCMPWCSGSIASSVCGWANSCTPIGYICEGRGCCL 807
QY 47 --LRMCTPLGR-----EGEECHPG-----SHKVPFFRKRKHTCPLCNLLCS 87
DB 808 EPLPLCPNGGRASMRGRCGCEPFGCTPLGCGLLSMPEVCPTRSNVAVCQSPNVVC- 866
QY 88 RFPDGRYRCSM 98
DB 867 --PSGA-SCTM 874
RESULT 4
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 08-Sep-2002
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564947
C:Genetics:
A:Gene: notch4
A:Map position: 17
A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
1679/3; 1729/1; 1761/3
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: receptor; signal transduction
F:514-545/Domain: EGF homology <EGF>

Query Match 13.8%; Score 81; DB 2; Length 1964;
Best Local Similarity 30.4%; Pred. No. 3.5;
Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;
QY 26 CERDQV-----CGAGTCCCAISLWRLGRLMCTPLGRGEECHPGSHKVPFFRKRKH 76
DB 188 CERDINECFLEPGPCPGTSGHNTL---GSVQCLCPVGQEGPQC-----KLRKG 233
QY 77 TCP-----CLPNLLCSRPDG 92
DB 234 ACPGSGCLNGGTCQLVPEG 252

RESULT 5

XLMU
collipase precursor [validated] - human
N:Alternate names: procollipase
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 08-Dec-2000
C:Accession: A42568; A33949; A03163
R:Sims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A:Title: The human collipase gene: isolation, chromosomal location, and tissue-specific
A:Reference number: A42568; MUID:92353041; PMID:1643046
A:Accession: A42568
A:Molecule type: DNA
A:Residues: 1-112 <SIM>
A:Cross-references: GB:M95529; NID:g180842; PIDN:AA05818.1; PID:g1483624
A:Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBIP:110580)
R:Lowe, M.E.; Rosenblum, J.L.; MCEwen, P.; Strauss, A.W.
Biochemistry 29, 823-828, 1990
A:Title: Cloning and characterization of the human collipase cDNA.
A:Reference number: A33949; MUID:90248429; PMID:2337598
A:Accession: A33949
A:Molecule type: mRNA
A:Residues: 1-112 <LOW>
A:Cross-references: GB:J02883; NID:g180885; PIDN:AAA52054.1; PID:g180886
A:Note: evidence of partial N-glycosylation, possibly at Asn-43
R:Sternby, B.; Engstrom, A.; Heilmann, U.; Viher, A.M.; Sternby, N.H.; Borgstrom, B.
Biochim. Biophys. Acta 784, 75-80, 1984
A:Title: The primary sequence of human pancreatic collipase.
A:Reference number: A90652; MUID:84104937; PMID:6691986
A:Accession: A03163
A:Molecule type: protein
A:Residues: 23-108 <STE>
C:Comment: Collipase, a cofactor of trisacylglycerol lipase (EC 3.1.1.3), forms a 1:1 sto
se the enzyme is washed off by bile salts, which are known to have an inhibitory effect
C:Genetics:
A:Gene: GDB:CLPS
A:Cross-references: GDB:127277; OMIM:120105
A:Map position: 6pter-6p21.1
A:Introns: 28/3; 69/3
C:Superfamily: collipase
C:Keywords: lipid digestion; lipid hydrolysis; pancreas
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-22/Domain: amino-terminal propeptide #status predicted <APP>
F:23-108/Product: collipase #status experimental <MAT>
F:109-112/Domain: carboxyl-terminal propeptide #status predicted <CPP>
F:34-104,40-56,44-80,45-78,66-86/Disulfide bonds: #status predicted
F:69,72,75,76/Binding site: micellar substrate (Lys, Tyr, Tyr) #status predicted

Query Match 13.4%; Score 79; DB 1; Length 112;
Best Local Similarity 28.4%; Pred. No. 0.52;
Matches 31; Conservative 9; Mismatches 45; Indels 24; Gaps 6;
QY 9 IMLLVTVSDCAVITG-----ACERDVCGAGTCCCAISLWRLGRLMCTPLGR 56
DB 5 LILLVVALSVAAFGPRGIINLENGELCMNSAQC-KSNCCQHSSAL-GLARCTSMASE 62
QY 57 GEECHPGSHKVPFFRKRKHTCPLCNLLCSRFPDGRYRCSDMLKKNIF 105
DB 63 NSEC---SVKTLV---GIYKPCPCERGLTC----EGDKTIVGSITNTNF 101

Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:G3449293; PIDN:BAA32462.1; PID:G3449294
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 12.8%; Score 75.5; DB 2; Length 1574;
Best Local Similarity 28.6%; Pred. No. 10;
Matches 24; Conservative 6; Mismatches 33; Indels 21; Gaps 4;

QY 19 CAVITGAC-----ERDVCGAGTCCCAISLWLRLMCTPLRGEGEGCHPGSHKVPFRKR 73
DB 755 CHRVTEGLCPGKGTGDCGAD--CPEGRWGLGCGEICPACBHGASCPD----- 801
QY 74 KHHTCPCLPNLLCSRFPPDGRYCS 97
DB 802 EGTGCLCLPGFVGSRCQD---TCS 822

RESULT 9
JC4861
fertilin beta chain - human
C:Species: Homo sapiens (man)
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 21-Jan-2000
A:Accession: JC4861
R:Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A:Title: Molecular cloning of the human fertilin beta subunit.
A:Reference number: JC4861; MUID:96295488; PMID:8702389
A:Accession: JC4861
A:Molecule type: mRNA
A:Residues: 1-734 <GUP>
A:Cross-references: GB:U38805; NID:G4151118; PIDN:AAD04206.1; PID:G4151119
C:Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C:Superfamily: mouse meltrin alpha, disintegrin homology
C:Keywords: glycoprotein; integrin binding; transmembrane protein
F:382-734/Product: fertilin beta chain #status predicted <NAT>
F:382-467/Domain: disintegrin homology <DIS>
F:448-450/Region: integrin binding #status predicted
F:686-708/Domain: transmembrane #status predicted <TM>
F:121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.7%; Score 75; DB 2; Length 734;
Best Local Similarity 28.8%; Pred. No. 6.2;
Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3;

QY 15 TVSDCAVITGAC-----ERDVCGAGTCCCAISLWLRLMCTPLRGEGEGCHPGSHK 66
DB 401 TEQDCALIGETCCDIATCRFKAGSNCAEGPCCCNCLFMSKERMCRP---SPEEC-----D 452
QY 67 VPFPRKRKHHTCP 79
DB 453 LPEYCNCGSSASCP 465

RESULT 10
S45306
notch 3 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
A:Accession: S45306
R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A:Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-
A:Reference number: S45306; MUID:95001556; PMID:7918097
A:Accession: S45306
A>Status: preliminary

Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: Z14126; MUID:98360089; PMID:9693030
A:Accession: T13954
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: EMBL:AB011532; NID:G3449293; PIDN:BAA32462.1; PID:G3449294
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match 12.8%; Score 75.5; DB 2; Length 1574;
Best Local Similarity 28.6%; Pred. No. 10;
Matches 24; Conservative 6; Mismatches 33; Indels 21; Gaps 4;

QY 19 CAVITGAC-----ERDVCGAGTCCCAISLWLRLMCTPLRGEGEGCHPGSHKVPFRKR 73
DB 755 CHRVTEGLCPGKGTGDCGAD--CPEGRWGLGCGEICPACBHGASCPD----- 801
QY 74 KHHTCPCLPNLLCSRFPPDGRYCS 97
DB 802 EGTGCLCLPGFVGSRCQD---TCS 822

RESULT 9
JC4861
fertilin beta chain - human
C:Species: Homo sapiens (man)
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 21-Jan-2000
A:Accession: JC4861
R:Gupta, S.K.; Alves, K.; O'Neil Palladino, L.; Mark, G.E.; Hollis, G.F.
Biochem. Biophys. Res. Commun. 224, 318-326, 1996
A:Title: Molecular cloning of the human fertilin beta subunit.
A:Reference number: JC4861; MUID:96295488; PMID:8702389
A:Accession: JC4861
A:Molecule type: mRNA
A:Residues: 1-734 <GUP>
A:Cross-references: GB:U38805; NID:G4151118; PIDN:AAD04206.1; PID:G4151119
C:Comment: This protein is an integral sperm membrane glycoprotein, and plays a role in
C:Superfamily: mouse meltrin alpha, disintegrin homology
C:Keywords: glycoprotein; integrin binding; transmembrane protein
F:382-734/Product: fertilin beta chain #status predicted <NAT>
F:382-467/Domain: disintegrin homology <DIS>
F:448-450/Region: integrin binding #status predicted
F:686-708/Domain: transmembrane #status predicted <TM>
F:121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.7%; Score 75; DB 2; Length 734;
Best Local Similarity 28.8%; Pred. No. 6.2;
Matches 21; Conservative 7; Mismatches 29; Indels 16; Gaps 3;

QY 15 TVSDCAVITGAC-----ERDVCGAGTCCCAISLWLRLMCTPLRGEGEGCHPGSHK 66
DB 401 TEQDCALIGETCCDIATCRFKAGSNCAEGPCCCNCLFMSKERMCRP---SPEEC-----D 452
QY 67 VPFPRKRKHHTCP 79
DB 453 LPEYCNCGSSASCP 465

RESULT 10
S45306
notch 3 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
A:Accession: S45306
R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A:Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-
A:Reference number: S45306; MUID:95001556; PMID:7918097
A:Accession: S45306
A>Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-2318 <LAR>
A:Cross-references: EMBL:X74760; NID:g483580; PIDN:CAA52776.1; PID:g483581
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:163-195/Domain: EGF homology <EGF1>
F:474-505/Domain: EGF homology <EGF1>
F:854-885/Domain: EGF homology <EGF2>
F:1833-1871/Domain: ankyrin repeat homology <AN1>
F:1872-1904/Domain: ankyrin repeat homology <AN2>
F:1906-1938/Domain: ankyrin repeat homology <AN3>
F:1938-1971/Domain: ankyrin repeat homology <AN4>
F:1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 12.7%; Score 75; DB 2; Length 2318;
Best Local Similarity 28.1%; Pred. No. 16;
Matches 25; Conservative 5; Mismatches 25; Indels 34; Gaps 5;

QY 19 CAVITGACRDVQCGAGTCCATSLWRLGLRMCTPLGREGEC-----60
Db 1287 CERVARSC-RELQCPVGIFCQQT--ARGPRCACPPGLSGPSCVSRASPSGATNASCASA 1343

QY 61 ----HPGSC----HKVPFFRKHKHTCPCLP 82
Db 1344 PCLHGSGCLPVGQSPVFFR-----CVCAP 1366

RESULT 11
T31070
notch homolog - sea urchin (Lytechinus variegatus)
C:Species: Lytechinus variegatus (variegated urchin)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: T31070
R:Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A:Title: Identification and localization of a sea urchin Notch homologue: insights into
A:Reference number: Z20966; MUID:97454256; PMID:9310331
A:Accession: T31070
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2531 <SHE>
A:Cross-references: EMBL:AF00634; NID:g2570350; PID:g2570351; PIDN:AA82088.1
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 12.7%; Score 75; DB 2; Length 2531;
Best Local Similarity 29.3%; Pred. No. 17;
Matches 23; Conservative 8; Mismatches 32; Indels 14; Gaps 5;

QY 22 ITGACERDVQCGAGTCCAT--SLWRLGLRMCTPLGREGECHPGSHKVPFFRKHKHTCP 79
Db 120 VDNVCKLEPCQNGGTCRLTSLWDYEC-FCIP-ANTGENCTDDHCV-----SNP 168

QY 80 CLPNLCSRFPDGRYRC 96
Db 169 CLNGAVCTSSDG-YSC 184

RESULT 12
I51909
collipase precursor - rat
N:Alternate names: procollipase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Apr-2000
C:Accession: I51909; A34623
R:Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.
Am. J. Physiol. 266, G914-G921, 1994
A:Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA
A:Reference number: I51909; MUID:94262798; PMID:8203536
A:Accession: I51909
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-112 <PAY>
A:Cross-references: GB:M58370; NID:g203504; PIDN:AAA20505.1; PID:g203505
R:Wicker, C.; Puigserver, A.

Biochem. Biophys. Res. Commun. 167, 130-136, 1990
A:Title: Rat pancreatic colipase mRNA: nucleotide sequence of a cDNA clone and nutrition
A:Reference number: A34623; MUID:90179738; PMID:2129524
A:Accession: A34623
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-17, 'V', 19-112 <WIC>
A:Cross-references: GB:M33333; NID:g203502; PIDN:AAA40943.1; PID:g203503
C:Superfamily: colipase
C:Keywords: lipid digestion; lipid hydrolysis; pancreas
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-112/Product: colipase #status predicted <MAT>

Query Match 12.6%; Score 74; DB 2; Length 112;

Best Local Similarity 25.8%; Pred. No. 1.7;
Matches 24; Conservative 10; Mismatches 39; Indels 20; Gaps 4;

QY 6 RVSIMLLLVTVSDCAVITG-----ACERDVQCGAGTCCATSLWRLGLRMCTPL 53
Db 2 KVLVLLVTLVAVAAAPGRLGFINLEDEGICVNSMQC-KSRCCQHDITL-GIARCTHK 59

QY 54 GREGECCHPGSHKVPFFRKHKHTCPCLPNLLC 86

Db 60 AMENSECSPKTLGIYR-----CPCERGLTC 86

RESULT 13

T27283

hypothetical protein Y64G10A.f - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27283

R:Ainscough, R.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20336

A:Accession: T27283

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1620 <WIL>

A:Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f

A:Experimental source: clone Y64G10A

C:Genetics:

A:Gene: CESP:Y64G10A.f

A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1;

Query Match 12.6%; Score 74; DB 2; Length 1620;

Best Local Similarity 27.5%; Pred. No. 15;

Matches 22; Conservative 4; Mismatches 16; Indels 38; Gaps 4;

QY 16 VSDCAVITGACERDVQCGAG-----TCCATSLWRLGLRMCTPLGREGECCHPGSHKVP 68

Db 1114 VARCDHVTGEC-----RCPAGWTGPDQCTSC-----PLGRHGEGC----- 1148

QY 69 FFRKHKHTCPCLPNLLCSR 88

Db 1149 -----RHSCQCQCSNGASCDR 1162

RESULT 14

A35356

tumor necrosis factor receptor 2 precursor [validated] - human

N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000

C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094

R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.

Science 248, 1019-1023, 1990

A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

A:Reference number: A35356; MUID:90260639; PMID:2160731

A:Accession: A35356

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <SMI>

A:Cross-references: GB:M32315; NID:q189185; PIDN:AAAS9929.1; PID:q189186
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A:Reference number: A36475; MUID:91045991; PMID:2172983
A:Accession: A36475
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-195, 'R', 197-461 <KOH>
A:Cross-references: GB:M55994; GB:M38549; NID:q339757; PIDN:AAA36755.1; PID:q339758
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A:Reference number: A48416; MUID:91370690; PMID:1966549
A:Accession: A48416
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 23-461 <DEM>
A:Cross-references: GB:S63368; NID:q235648; PIDN:AABI19824.1; PID:q235649
A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A:Reference number: A36007; MUID:90349572; PMID:2166946
A:Accession: A36007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A:Cross-references: GB:M35857; NID:q339751; PIDN:AAA63262.1; PID:q339752
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A:Reference number: A23666; MUID:91056048; PMID:2173696
A:Accession: A23666
A:Status: preliminary
A:Molecule type: protein
A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: B35010
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-31 <ENG>
R:Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
A:Reference number: I38094; MUID:95121934; PMID:7821811
A:Accession: I38094
A:Status: preliminary; translated from GB/EMBL/DBJ
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A:Residues: 1-37 <RES>
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A:Cross-references: GDB:125914; OMIM:191191
A:Map position: lp36.2-lp36.2
A:Introns: 28/3
A:Note: the list of introns is incomplete
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98 SRCSSDQVETQACTREQNRICTCRPEWYCAJSK-OEGRLCAPLRKCRPGFGVAPGTET 156
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QY 60 -----CHPGSHKVPFFFRKRKHHTCPCLPNLLCS 87
157 SDVCKPCAPGT-----FSNTTSTSDICRPHQICN 186
Db
RESULT 15
S14458
laminin alpha-1 chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 19-Jan-2001
C:Accession: S14458; S14663; A34961
R:Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.
Matrix 11, 151-160, 1991
A:Title: Molecular cloning of the cDNA encoding human laminin A chain.
A:Reference number: S14458; MUID:91333420; PMID:1714537
A:Accession: S14458
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3075 <HAA>
R:Nissinen, M.; Vuolteenaho, R.; Boot-Handford, R.; Kallunki, P.; Tryggvason, K.
Biochem. J. 276, 369-379, 1991
A:Title: Primary structure of the human laminin A chain. Limited expression in human tis
A:Reference number: S14663; MUID:91264789; PMID:2049067
A:Accession: S14663
A:Molecule type: mRNA
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A:Cross-references: EMBL:X58531; NID:G34225; PIDN:CAA41418.1; PID:G34226
R:Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A:Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 ch
A:Reference number: A34961; MUID:89280632; PMID:2733383
A:Accession: A34961
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'W', 2397-2745, 'L', 2747-3053, 'L', 3055-3072, 'PSP', <OLS>
A:Note: the authors translated the codon AGA for residue 2692 as Pro
C:Genetics:
A:Gene: GDB:LAMAL1; LAMA
A:Cross-references: GDB:120135; OMIM:150320
A:Map position: lp31.32-lp31.22
C:Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like r
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; disulfide bo
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F:2323-2484/Domain: laminin G repeat homology <LG2>
F:2510-2676/Domain: laminin G repeat homology <LG3>
F:2534-2536/Region: cell attachment (R-G-D) motif
F:2739-2888/Domain: laminin G repeat homology <LG4>
F:2916-3073/Domain: laminin G repeat homology <LG5>
F:38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1
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F:297-305/Disulfide bonds: #status predicted

Query Match 12.4%; Score 73; DB 2; Length 3075;
Best Local Similarity 23.0%; Pred. No. 32;
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DB 1056 CDVVTGHCQCKSKFGGRACDQCGLGYRDFPDCVPCDCLRGTSGDACNLEQGLCGCVET 1115

QY 63 GSHKVPFFPKRKHHHTCPCLPNLL---CSRFPDGRYRCMD 99
DB 1116 GA-----CPCKENVFGQCNECREGTFAIRAD 1142

Search completed: January 12, 2004, 13:35:41
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:32:21 ; Search time 41 Seconds
(without alignments)
406.495 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVSMILLVTVSDCA.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	589	100.0	105	21 AAB18453 A human TANGO 266
2	589	100.0	105	21 AAY66745 Membrane-bound pro
3	589	100.0	105	22 AAU12406 Human PRO1186 poly
4	589	100.0	105	22 AAB68427 Amino acid sequenc
5	589	100.0	105	22 AAB70148 Human G protein-co
6	589	100.0	105	22 AAB48175 Human PRO1186 poly
7	589	100.0	105	22 AAB65268 Human PRO1186 (UNQ
8	589	100.0	105	22 AAB48067 Human extracellular
9	589	100.0	105	22 AAB53096 Human angiogenesis

10	589	100.0	105	23 AAO15527 Human physiological
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16	589	100.0	105	23 AAM50773 Endocrine gland-de
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18	589	100.0	105	24 ABU66804 Human endocrine gl
19	589	100.0	105	24 ABU67080 Human secreted/tr
20	589	100.0	105	24 ABU07603 Human ZVEN2. Homo
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22	589	100.0	105	24 ABUS9161 Novel human secret
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27	589	100.0	105	24 ABUS9014 Human secreted/tr
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33	588	99.8	105	23 AAO15526 Human physiological
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43	541	91.9	105	23 ABB99153 Rat ZAQ protein.
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ALIGNMENTS

RESULT 1

AAB18453

ID AAB18453 standard; Protein; 105 AA.

XX AC AAB18453;

XX DT 15-JAN-2001 (first entry)

XX DE A human TANGO 266 polypeptide.

XX KW TANGO 266; TANGO 216;; TANGO 261; TANGO 262; TANGO 267;

XX KW cellular proliferation; cellular differentiation; cellular adhesion;

XX KW von Willebrand factor-associated disorder; cell trafficking; cancer;

XX KW hematopoietic associated disease; atelectasis; pulmonary congestion;

XX KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;

XX KW intestinal disorder; spleen associated disease; renal disorder;

XX KW cardiovascular disorder; ischemic heart disease; hydrocephalus;

XX KW brain herniation; itrogenic disease; inflammation; meningitis;

XX KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;

XX KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers

XX FT Peptide 1..19

XX FT Protein /note= "signal sequence"

XX FT /note= "mature protein"

XX FT WO200052022-A1.

XX FT 08-SEP-2000.

XX PD

XX 01-MAR-2000; 2000WO-US05226.
PF
XX 01-MAR-1999; 99US-0122458.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
PI
XX WPI; 2000-579269/54.
DR N-PSDB; AAA75155.
XX
XX Novel human and murine secreted proteins designated TANGO 216, 261,
PT 262, 266 and 267 useful as modulating agents of cellular processes,
PT e.g. for treating cancer -
XX
XX Claim 8; Fig 14; 175pp; English.
XX
XX The present sequence represents a human TANGO 266 polypeptide. The
CC specification also describes TANGO 262, TANGO 216, TANGO 261, and
CC TANGO 267. The TANGO polypeptides can be used to modulate cellular
CC proliferation, modulate cellular differentiation and/or modulate
CC cellular adhesion. The proteins can be used to treat any von Willebrand
CC factor-associated disorder, regulate extracellular matrix structuring,
CC cellular adhesion, and cell trafficking and/or migration, modulate
CC cellular interactions, modulate cell adhesion in proliferative
CC disorders, such as cancer, modulate the proliferation, differentiation,
CC and/or function of cells that appear in the bone marrow, and leukocytes,
CC treat bone marrow, blood and hematopoietic associated diseases and
CC disorders, atelectasis, pulmonary congestion or oedema, emphysema,
CC chronic bronchitis, bronchial asthma and bronchiectasis, intestinal
CC disorders, spleen associated diseases, modulate renal disorders, treat
CC cardiovascular disorders such as ischemic heart disease, modulate the
CC proliferation, differentiation, and/or function of bone and cartilage
CC cells and to treat bone and/or cartilage associated diseases or
CC disorder. They may also be used to treat disorders associated with the
CC ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic
CC disease, inflammations, bacterial and viral meningitis, Alzheimer's
CC disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis,
CC brain cancers, hydrocephalus and encephalitis, and treat hepatic
CC disorders.
XX
XX Sequence 105 AA;
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Best Local Similarity 100.0%; Pred. No. 9.2e-56;
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QY 61 HPGSHKVPFRKRKHHTCPCLPNLLCSRFPDGRYCSMDLKNINF 105
Db 61 HPGSHKVPFRKRKHHTCPCLPNLLCSRFPDGRYCSMDLKNINF 105
RESULT 2
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DT 05-APR-2000 (first entry)
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XX Membrane-bound protein PRO1186.
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XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
XX
XX WO9963088-A2.
PN

XX 09-DEC-1999.
PD
XX 02-JUN-1999; 99WO-US12252.
PF
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PR

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PR 12-JAN-1999; 99US-0115565.
XX (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
```

XX WPI; 2000-072883/06.
DR N-PSDB; AA265091.
XX Membrane-bound proteins and related nucleotide sequences -
XX claim 12; Fig 266; 822pp; English.
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX Sequence 105 AA;
SQ

Query Match 100.0%; Score 589; DB 21; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGREGSC 60
|||
Db 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLRGREGSC 60
|||
QY 61 HPGSHKVPFFRKRRKHHTCPCLPNLLCSRPDGRYRCMDLKNINF 105
|||
Db 61 HPGSHKVPFFRKRRKHHTCPCLPNLLCSRPDGRYRCMDLKNINF 105
|||

RESULT 3
AAU12406
ID AAU12406 standard; Protein; 105 AA.
XX
AC AAU12406;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO1186 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 02-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.

```
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Deenoyers L, Filvaroff E, Gao W;
PI Gerritsen WB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2001-408281/43.
XX N-PSDB; AAS21478.
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
XX Claim 12; Fig 470; 813pp; English.
XX
XX AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX
XX Sequence 105 AA;
SQ
Query Match 100.0%; Score 589; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCALSLWRLGLRMCTPLGRGEEC 60
DB 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCALSLWRLGLRMCTPLGRGEEC 60
QY 61 HPGSHKVPFFRKRGKHTTCPLNLLCSRRFPDGRYRCMDLKNINF 105
DB 61 HPGSHKVPFFRKRGKHTTCPLNLLCSRRFPDGRYRCMDLKNINF 105
XX
XX RESULT 4
XX AAB68427
XX AAB68427 standard; Protein; 105 AA.
XX
XX AAB68427;
XX
```

```
XX 23-JUL-2001 (first entry)
XX
XX Amino acid sequence of a human Zven2 polypeptide.
XX
XX Zven1; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing;
KW antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme;
KW cellular differentiation; gastrointestinal cell contractility;
KW gastrointestinal motility; inflammation; hypermotility; diarrhoea;
KW Crohn's disease.
XX
XX Homo sapiens.
XX
XX WO200136465-A2.
XX
XX 25-MAY-2001.
XX
XX 14-NOV-2000; 2000WO-US31278.
XX
XX 16-NOV-1999; 99US-0442164.
XX 25-FEB-2000; 2000US-0511879.
XX 19-APR-2000; 2000US-0552203.
XX 07-JUN-2000; 2000US-0210332.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Bishop PD, Whitmore TE, Thompson PP;
PI
XX WPI; 2001-355611/37.
XX N-PSDB; AAF85427.
XX
XX Novel isolated Zven polypeptide useful for inhibiting proliferation of
PT tumour cells, for treating small cell cancer of lung, to promote wound
PT healing, and for treating Crohn's disease and diarrhoea
XX
XX Claim 27; Page 4; 98pp; English.
XX
XX The present sequence represents a human Zven2 polypeptide. The
CC specification also describes Zven1. The Zven1 gene is present on
CC chromosome 3p21.1-3p14.3. The specification also describes Zven2. Zven
CC polynucleotides and polypeptides are useful in veterinary and human
CC therapeutics, for treating small cell cancer of the lung, to promote
CC wound healing, to prevent or to treat an adverse reaction of the skin
CC to a skin-sensitizing agent or a skin-irritating agent, to stimulate
CC the immune system of an immunocompromised individual, as antitumour
CC agents, as antiinflammatory agents, as agents to regulate regeneration
CC or remodeling of tissue, as agents to modulate necrosis or tissue
CC growth developmental arrest, to inhibit proliferation of tumour cells,
CC cellular differentiation and necrosis, to treat disorders associated
CC with gastrointestinal cell contractility, secretion of digestive
CC enzymes and acids, gastrointestinal motility, recruitment of digestive
CC enzymes, inflammation, and conditions associated with hypermotility
CC such as diarrhoea and Crohn's disease.
XX
XX Sequence 105 AA;
SQ
Query Match 100.0%; Score 589; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCALSLWRLGLRMCTPLGRGEEC 60
DB 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCALSLWRLGLRMCTPLGRGEEC 60
QY 61 HPGSHKVPFFRKRGKHTTCPLNLLCSRRFPDGRYRCMDLKNINF 105
DB 61 HPGSHKVPFFRKRGKHTTCPLNLLCSRRFPDGRYRCMDLKNINF 105
XX
XX RESULT 5
XX AAB70148
XX AAB70148 standard; Protein; 105 AA.
XX
```

AC AAB70148;
XX 29-MAY-2001 (first entry)
XX Human G protein-coupled receptor protein-related sequence #4.
DE
XX Human; G protein-coupled receptor protein; neotropic; neuroprotective;
KW hypotensive; orexigenic; antiallergic; antianginal; antimicrobial;
KW antibacterial; gene therapy; Alzheimer's disease; hypertension;
KW anorexia; allergy; angina pectoris; infection; MRSa;
KW multiple resistant Staphylococcus aureus.
OS Homo sapiens.
XX WO200116309-A1.
PN 08-MAR-2001.
PD
XX 24-AUG-2000; 2000WO-JP05685.
XX 27-AUG-1999; 99JP-0241531.
PR 18-JUL-2000; 2000JP-0217474.
XX (TAKE) TAKEDA CHEM IND LTD.
PA Watanabe T, Terao Y, Shintani Y;
PI WPI; 2001-226684/23.
DR
XX New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
PT hypertension and anorexia -
XX Example 4; Page 113; 119pp; Japanese.
PS
XX The present sequence is provided in a specification relating to a
CC protein or its salt with an amino acid sequence identical or
CC substantially similar to a fully defined sequence of 393 amino acids as
CC given in the specification. The protein is useful in gene diagnosis and
CC development of preventives and remedies for diseases associated with
CC dysfunction of the protein, e.g. Alzheimer's disease, hypertension,
CC anorexia, allergy, angina pectoris and infections (e.g. multiple
CC resistant Staphylococcus aureus. The proteins and DNA encoding the
CC proteins are also useful for the treatment of these diseases by gene
CC therapy.
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGEC 60
Db 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGEC 60
QY 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRFPDGRYRCSMDLKNINF 105
Db 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRFPDGRYRCSMDLKNINF 105
RESULT 6
AAB48175
ID AAB48175 standard; Protein; 105 AA.
XX AAB48175;
AC
XX 02-APR-2001 (first entry)
DT Human PRO1186 polypeptide.
DE
XX PRO1186; PRO184; neoplastic; cell growth; tumour; cancer; breast;

KW ovarian; renal; colorectal; uterine; prostate; lung; melanoma;
KW central nervous system; leukemia; antitumor; cytostatic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "signal sequence"
FT Protein /note= "mature protein"
FT Modified-site 33..39 /note= "N-myristoylation site"
FT Modified-site 35..41 /note= "N-myristoylation site"
FT Modified-site 46..52 /note= "N-myristoylation site"
FT Modified-site 88..95 /note= "tyrosine kinase phosphorylation site"
XX WO200075327-A1.
PN 14-DEC-2000.
PD
XX 24-FEB-2000; 2000WO-US04914.
XX 02-JUN-1999; 99WO-US12252.
PR 26-JUL-1999; 99US-0145698.
PR 05-JAN-2000; 2000WO-US00219.
XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Hillan KJ, Napier MA, Watanabe CK, Wood WI;
PI WPI; 2001-071078/08.
DR N-PSDB; AAC84469.
XX
PT Compositions for inhibiting neoplastic cell growth and treating tumor,
PT a cancer, comprises novel PRO1186 or PRO184 polypeptides or its agonist
PT -
XX Claim 31; Fig 2; 104pp; English.
PS
XX The invention provides PRO1186 and PRO184 polypeptides that can be used
CC for the inhibition of neoplastic cell growth and for treating tumours.
CC The PRO polypeptides can be expressed by standard recombinant
CC methodology. The PRO polypeptides or their agonists are useful for
CC inhibition of neoplastic cell growth and for treating tumours, cancers
CC such as breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder or central nervous system cancers or melanoma and leukemia. The
CC present sequence represents the human PRO1186 polypeptide (encoding
CC CDNA clone ID: DNA60621-1516).
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGEC 60
Db 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGREGEC 60
QY 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRFPDGRYRCSMDLKNINF 105
Db 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRFPDGRYRCSMDLKNINF 105
RESULT 7
AAB65268
ID AAB65268 standard; Protein; 105 AA.
XX AAB65268;
AC
XX

DT 02-APR-2001 (first entry)

XX Human PRO1186 (UN0600) protein sequence SEQ ID NO:371.

DE Human; secreted and transmembrane protein; PRO; cytosolic;

XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;

KW diagnostic assay.

KW Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 08-OCT-1999; 99US-0158563.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28301.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 02-MAR-2000; 2000WO-US05841.

PR 15-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

XX (GETH) GENENTECH INC.

XX Ashtenazi AJ, Baker KP, Botstein D, Deanoyers L, Eaton DL;

XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi CJ, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;

XX WPI: 2001-032160/04.

DR N-PSDB; AAF44237.

XX PRO polynucleotides used to produce polypeptides used to target

PT bioactive molecules such as toxins, radiolabels or antibodies, to

PT specific cells, to cause targeted cell death -

XX Claim 12; Fig 266; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO

XX proteins. The PRO proteins have cytostatic activity. The PRO proteins

CC can be used for targeted delivery of bioactive molecules, such as

CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

CC sequences, and their fragments, can be used as hybridisation probes in

CC chromosomal and gene mapping, and in the generation of anti-sense RNA

CC and DNA. They may also be used to produce transgenic animals which are

CC used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in

CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.

CC AAF44270 to AAF4470 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and

CC AAF65154 to AAF65300 represent human PRO polynucleotide and protein

XX sequences given in the exemplification of the present invention.

SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 22; Length 105;

Best Local Similarity 100.0%; Pred. No. 9.2e-56;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRNCTPLRGREGBC 60

DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRNCTPLRGREGBC 60

QY 61 HPGSHKVPFFRKRRKHTCTCPLNLLCSRFPDGRYRCSMDLKNINF 105

DB 61 HPGSHKVPFFRKRRKHTCTCPLNLLCSRFPDGRYRCSMDLKNINF 105

RESULT 8

AAB48067

ID AAB48067 standard; protein; 105 AA.

XX AC AAB48067;

XX DT 19-MAR-2001 (first entry)

XX DE Human extracellular signaling molecule (EXCS) (ID 2006548CD1).

XX KW Extracellular signaling molecule; EXCS; anti-inflammatory; human;

XX KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;

XX KW virucide; antibacterial; anti-HIV; human immunodeficiency virus;

XX KW antifertility; cerebroprotective; nootropic; antileukemic; antifungal;

XX KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;

XX KW keratolytic; protozoicide; gene therapy.

XX OS Homo sapiens.

XX FN WO200070049-A2.

XX PD 23-NOV-2000.

XX PF 19-MAY-2000; 2000WO-US13975.

XX PR 19-MAY-1999; 99US-0134949.

PR 15-JUL-1999; 99US-0144270.

PR 30-JUL-1999; 99US-0146700.

PR 04-OCT-1999; 99US-0157508.

XX (INCY-) INCYTE GENOMICS INC.

XX Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;

PI Azimzai Y, Lu DAN, Patterson C;

XX WPI: 2001-025021/03.

DR N-PSDB; AAC84303.

XX New human extracellular signaling nucleic acids and polypeptides useful

PT for diagnosing, treating and preventing infections and

PT gastrointestinal, neurological, reproductive, and

PT autoimmune/inflammatory disorders -

XX Claim 1; Page 89; 114pp; English.

XX The invention provides human extracellular signaling molecules (EXCS)

CC and polynucleotides which identify and encode EXCS. EXCS can be

CC expressed by standard recombinant methodology. The amino acid and nucleic

CC acid sequences of EXCS are useful for diagnosing, treating and

CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,

CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular

CC disease, stroke), reproductive (infertility, ovulatory defects,

CC endometriosis), autoimmune /inflammatory (actinic keratosis, and cell

CC immunodeficiency syndrome (AIDS), Addison's disease), and cell

CC proliferative disorders including cancers (of the breast, adrenal gland,

CC bone). They may also be used to treat fatal familial insomnia,

CC nutritional and metabolic diseases of the nervous system, myopathies,

CC mental disorders (anxiety, schizophrenia, mood), as well as infections

CC caused by parasites (malaria, leishmania, trypanosoma), viral
 CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,
 CC staphylococcus, bacillus), and fungal (aspergillus, blastomycetes,
 CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,
 CC agonists, pharmaceutical compositions, and antibodies may also be used
 CC for treating or preventing disorders associated with increased or
 CC decreased expression or quantity of EXCS. EXCS polynucleotides may also
 CC be used to detect and identify gene expression in biopsied tissues in
 CC which expression of EXCS may be correlated with the disease, to determine
 CC presence or excess expression of EXCS, to monitor regulation of EXCS
 CC levels during therapeutic intervention, to detect the presence of
 CC associated disorders, as targets in microarray, to generate hybridization
 CC probes, and to detect differences in gene sequences among normal, carrier
 CC or affected individuals. Antibodies may also be used in diagnosing
 CC disorders, in monitoring patients being treated with EXCS agonists,
 CC antagonists or inhibitors. Sequences AAB48057-B48082 represent the EXCS
 CC of the invention.
 XX
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 589; DB 22; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.2e-56;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
 Db 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
 QY 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
 Db 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
 RESULT 9
 AAB53096
 ID AAB53096 standard; Protein; 105 AA.
 XX
 XX
 AC AAB53096;
 DT 28-FEB-2001 (first entry)
 DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.
 XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 PN WO200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US00219.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.

PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX
 XX WPI: 2001-090793/10.
 DR N-PSDB; AAC97496.
 XX
 XX New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or
 PT angiogenic disorders, such as atherosclerosis, wounds or cancer -
 XX
 PS Claim 69; Fig 66; 293pp; English.
 XX
 CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof.
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic
 CC animals useful for the development and screening of potential
 CC therapeutic agents. The present sequence represents a PRO protein of the
 CC invention.
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 589; DB 22; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.2e-56;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
 Db 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
 QY 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
 Db 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPDGRYRCSDMLKNINF 105
 RESULT 10
 AAO15527
 ID AAO15527 standard; Protein; 105 AA.
 XX
 XX AAO15527;
 AC AAO15527;
 XX
 XX 24-OCT-2002 (first entry)
 DT
 XX

DE Human physiologically-active ZAQ ligand-related protein 3.
XX
KW Human; ZAQ ligand; physiologically-active ZAQ ligand;
KW digestive disease; colitis; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200257443-A1.
XX
PD 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-JP00378.
XX
PF 22-JAN-2001; 2001JP-0013027.
PR 17-MAY-2001; 2001JP-0147759.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Yamada T, Suenaga M, Nishimura O;
PI
XX WPI; 2002-566801/60.
DR

XX Industrial production of physiologically-active ZAQ ligand by
PT expressing in transformant prokaryote and refolding in redox buffer,
PT for use in preventing or treating digestive diseases e.g. colitis and
PT diarrhea
XX
XX Example 3; Page 76-77; 93pp; Japanese.
XX
XX The invention comprises a method for producing an active peptide that has
XX the same activity as a ZAQ ligand isolated from eukaryotic cells. The
XX method of the invention is useful for the production of a
XX physiologically-active ZAQ ligand for use in preventing or treating
XX digestive diseases (e.g. colitis and diarrhea). The present amino acid
XX sequence represents a human physiologically active ZAQ ligand-related
XX protein.
XX
XX Sequence 105 AA;
SQ

Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
DB 1 MRGATVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFFRKXKHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105
DB 61 HPGSHKVPFFRKXKHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105

RESULT 11
AAE24382
ID AAE24382 standard; Protein; 105 AA.
XX
AC AAE24382;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human prokineticin 1 precursor protein.
XX
XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;
KW inflammatory bowel disorder; analgesic; infectious disease.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide 20..105

/note= "Mature human prokineticin 1"

FT XX WO200236625-A2.
PN XX 10-MAY-2002.
PD XX
XX
XX 01-NOV-2001; 2001WO-US47969.
XX
XX 03-NOV-2000; 2000US-245882P.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Zhou Q, Ehlert FJ;
PI
XX WPI; 2002-479752/51.
DR N-PSDB; AAD39321.
XX
XX New isolated human prokineticin 1 and 2 polypeptides that stimulate
PT gastrointestinal smooth muscle contraction, useful for improving
PT impaired gastrointestinal motility in irritable bowel syndrome, chronic
PT constipation
XX

Example 1; Fig 1; 86pp; English.

XX The invention relates to human prokineticin 1 and 2 polypeptides that
XX stimulate gastrointestinal smooth muscle contraction and nucleic acid
XX molecules encoding such polypeptides. Polypeptides of the invention
XX are useful for treating disorders involving impaired gastrointestinal
XX motility. They are useful for stimulating gastrointestinal motility
XX in disorders such as irritable bowel syndrome, diabetic gastroparesis,
XX post-operative ileus, chronic constipation and gastrointestinal
XX reflux disease. The prokineticin antagonists are useful for inhibiting
XX gastrointestinal motility in conditions of diarrhoea, malabsorptive
XX disorders, inflammatory bowel disorders, infectious diseases and
XX intestinal cancer. The antagonists also act as analgesics. The present
XX sequence is human prokineticin 1 precursor protein.
XX
XX Sequence 105 AA;
SQ

Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
DB 1 MRGATVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFFRKXKHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105
DB 61 HPGSHKVPFFRKXKHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105

RESULT 12
ABB95508
ID ABB95508 standard; Protein; 105 AA.
XX
AC ABB95508;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO1186 SEQ ID NO: 172.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
XX Homo sapiens.
OS
XX
XX WO200208284-A2.
XX
XX 31-JAN-2002.
PD
XX

PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220624P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001US-0806520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95646.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX
PS Claim 11; Fig 172; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGERC 60
DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGERC 60
QY 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRFPPDGRYRCSDMLKNINF 105
DB 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRFPPDGRYRCSDMLKNINF 105
RESULT 13
ABB06308
ID ABB06308 standard; Protein; 105 AA.
XX
AC ABB06308;
XX
DT 27-MAY-2002 (first entry)
XX
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.
XX
KW G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;
KW colitis; diarrhoea; constipation; poor-absorption syndrome;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200206483-A1.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-JP06162.
XX
PR 18-JUL-2000; 2000JP-0217442.
PR 02-FEB-2001; 2001JP-0026779.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
PI Hinuma S;
XX
XX WPI; 2002-188546/24.
DR N-PSDB; ABL49637.
XX
PT Physiologically-active peptides from cows milk, useful for developing
PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
PT like colitis, diarrhoea, constipation and poor-absorption syndrome, by
PT gene therapy -
XX
PS Claim 5; Page 61; 191pp; Japanese.
XX
CC The present invention describes a peptide containing an amino acid
CC sequence (I) identical to or substantially similar to that of the
CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic
CC and laxative activities. The peptides and encoding DNAs from the
CC present invention are useful for developing drugs to treat digestive
CC diseases like colitis, diarrhoea, constipation and poor-absorption
CC syndrome, including gene therapy. The physiologically-active cows
CC milk-originated peptides are applicable as a specific ligand of
CC brain-originated orphan G protein-coupled receptor protein ZAQ.
CC ABL49615 to ABB40659 and ABB06303 to ABB06315 represent sequences
CC used in the exemplification of the present invention.

```
XX SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9,2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLGREGEC 60
Db 1 MEGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLGREGEC 60
QY 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105
Db 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105

RESULT 14
ABB84902
ID ABB84902 standard; Protein; 105 AA.
AC ABB84902;
XX
XX
XX 16-MAY-2002 (first entry)
XX
XX Human PRO1186 protein sequence SEQ ID NO:172.
XX
XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
XX WO200200690-A2.
XX
XX 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US233522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242923P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 28-FEB-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 01-MAR-2001; 2001WO-US066520.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 03-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.
XX 25-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001US-0866028.
PR
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PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerecht ME, Goddard A;
PI Godowski RJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
XX N-PSDB; ABL88157.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 172; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal.
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX
XX SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9,2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLGREGEC 60
Db 1 MEGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTPLGREGEC 60
QY 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105
Db 61 HPGSHKVPFFRKHKHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105

RESULT 15
AAU83674
ID AAU83674 standard; Protein; 105 AA.
XX
XX AAU83674;
XX
XX 08-MAY-2002 (first entry)
XX
XX Human PRO protein, Seq ID No 166.
XX
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
PR
```

XX 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-172001/22.
DR N-PSDB; ABK3618.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
PS Claim 11; Figure 166; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
Db 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
QY 61 HPGSHKVPFFRKRKHHKTCPLNLLCSRFPPDGRYRCMDLKNINF 105
Db 61 HPGSHKVPFFRKRKHHKTCPLNLLCSRFPPDGRYRCMDLKNINF 105

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2	2	PRIOR FILING DATE: 1997-11-12	2
3	3	PRIOR APPLICATION NUMBER: 60/065311	3
4	4	PRIOR FILING DATE: 1997-11-13	4
5	5	PRIOR APPLICATION NUMBER: 60/066770	5
6	6	PRIOR FILING DATE: 1997-11-24	6
7	7	PRIOR APPLICATION NUMBER: 60/075945	7
8	8	PRIOR FILING DATE: 1998-02-25	8
9	9	PRIOR APPLICATION NUMBER: 60/078910	9
10	10	PRIOR FILING DATE: 1998-03-20	10
11	11	PRIOR APPLICATION NUMBER: 60/083322	11
12	12	PRIOR FILING DATE: 1998-04-28	12
13	13	PRIOR APPLICATION NUMBER: 60/084600	13
14	14	PRIOR FILING DATE: 1998-05-07	14
15	15	PRIOR APPLICATION NUMBER: 60/087106	15
16	16	PRIOR FILING DATE: 1998-05-28	16
17	17	PRIOR APPLICATION NUMBER: 60/087607	17
18	18	PRIOR FILING DATE: 1998-06-02	18
19	19	PRIOR APPLICATION NUMBER: 60/087609	19
20	20	PRIOR FILING DATE: 1998-06-02	20
21	21	PRIOR APPLICATION NUMBER: 60/087759	21
22	22	PRIOR FILING DATE: 1998-06-02	22
23	23	PRIOR APPLICATION NUMBER: 60/087827	23
24	24	PRIOR FILING DATE: 1998-06-03	24
25	25	PRIOR APPLICATION NUMBER: 60/088021	25
26	26	PRIOR FILING DATE: 1998-06-04	26
27	27	PRIOR APPLICATION NUMBER: 60/088025	27
28	28	PRIOR FILING DATE: 1998-06-04	28
29	29	PRIOR APPLICATION NUMBER: 60/088026	29
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31	31	PRIOR APPLICATION NUMBER: 60/088028	31
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33	33	PRIOR APPLICATION NUMBER: 60/088029	33
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35	35	PRIOR APPLICATION NUMBER: 60/088326	35
36	36	PRIOR FILING DATE: 1998-06-04	36
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39	39	PRIOR APPLICATION NUMBER: 60/088202	39
40	40	PRIOR FILING DATE: 1998-06-05	40
41	41	PRIOR APPLICATION NUMBER: 60/088212	41
42	42	PRIOR FILING DATE: 1998-06-05	42
43	43	PRIOR APPLICATION NUMBER: 60/088734	43
44	44	PRIOR FILING DATE: 1998-06-10	44
45	45	PRIOR APPLICATION NUMBER: 60/088738	45
46	46	PRIOR FILING DATE: 1998-06-10	46
47	47	PRIOR APPLICATION NUMBER: 60/088742	47
48	48	PRIOR FILING DATE: 1998-06-10	48
49	49	PRIOR APPLICATION NUMBER: 60/088810	49
50	50	PRIOR FILING DATE: 1998-06-10	50
51	51	PRIOR APPLICATION NUMBER: 60/088824	51
52	52	PRIOR FILING DATE: 1998-06-10	52
53	53	PRIOR APPLICATION NUMBER: 60/088826	53
54	54	PRIOR FILING DATE: 1998-06-10	54
55	55	PRIOR APPLICATION NUMBER: 60/088858	55
56	56	PRIOR FILING DATE: 1998-06-11	56
57	57	PRIOR APPLICATION NUMBER: 60/088861	57
58	58	PRIOR FILING DATE: 1998-06-11	58
59	59	PRIOR APPLICATION NUMBER: 60/088876	59
60	60	PRIOR FILING DATE: 1998-06-11	60
61	61	PRIOR APPLICATION NUMBER: 60/089105	61
62	62	PRIOR FILING DATE: 1998-06-12	62
63	63	PRIOR APPLICATION NUMBER: 60/089440	63
64	64	PRIOR FILING DATE: 1998-06-16	64
65	65	PRIOR APPLICATION NUMBER: 60/089512	65

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/ PRIOR APPLICATION NUMBER: 60/091360
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091478
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091544
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091519
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091626
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091633
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MGRATRVSTMLLLVTVSDCAVITGACERDVQCAGTCCCAISLWRLGLRMCCTPLRGEGRC 60
Db      1 MGRATRVSTMLLLVTVSDCAVITGACERDVQCAGTCCCAISLWRLGLRMCCTPLRGEGRC 60

QY      61 HPGSHKVPFFRRKRGKHTCCLNLLCSRPDPDGRYCSMDLKNINF 105
Db      61 HPGSHKVPFFRRKRGKHTCCLNLLCSRPDPDGRYCSMDLKNINF 105

RESULT 2
US-09-989-723-371
/ Sequence 371, Application US/09989723
/ Patent No. US20020072092A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
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/ APPLICANT: Gerritsen, Mary E.
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/ APPLICANT: Gurney, Austin L.
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/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
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/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730PIC62
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/ CURRENT FILING DATE: 2001-11-19
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEEC 60

Qy 61 HPGSHKVPFFRRKRKHHTCPCLENLLCSRPFDGRCSDMLKKNIF 105
Db 61 HPGSHKVPFFRRKRKHHTCPCLENLLCSRPFDGRCSDMLKKNIF 105

RESULT 3
US-09-989-279-371
; Sequence 371, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
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; PRIOR FILING DATE: 1997-06-16
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[illegible]

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Query Match 100.0%; Score 589; DB 9; Length 105;
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 Qy 61 HPGSHKVPFRKXKHTCPLNLLCSRFPDGRYRCMDLKNINF 105
 Db 61 HPGSHKVPFRKXKHTCPLNLLCSRFPDGRYRCMDLKNINF 105

RESULT 4

US-09-989-727-371
 ; Sequence 371, Application US/09989727
 ; Patent No. US20020072497A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: F2730P1C65
 ; CURRENT APPLICATION NUMBER: US/09/989, 727
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 1.9e-55;
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Db 61 HPGSHKVPFFRKHKHHTCPLNLLCSRRFPDGRYRCSMDLKNINF 105

RESULT 5
US-09-989-731-371
; Sequence 371, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerbet, Hanspeter
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 371, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumaas, Daniel
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
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Query Match 100.0%; Score 589; DB 10; Length 105;
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RESULT 8

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; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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136 PRIOR FILING DATE: 1998-07-07
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138 PRIOR FILING DATE: 1998-07-07
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Query Match 100.0%; Score 589; DB 10; Length 105;

Best Local Similarity 100.0%; Pred.No.1.9e-55;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 HPGSHKVPFRKRKHHTKCLNLLCSRPDPDGRYRCSDMLKKNIF 105

RESULT 10
US-09-993-604-371
Sequence 371, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
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63 PRIOR APPLICATION NUMBER: 60/092182
64 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 HPGSHKVPFFRRKRKHTCTCLPNNLLCSRRFPDGRYRCSMDLKNINF 105
RESULT 11
US-09-990-456-371
Sequence 371, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
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57	PRIOR FILING DATE: 1998-07-07	
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59	PRIOR FILING DATE: 1998-07-07	
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61	PRIOR FILING DATE: 1998-07-09	

Query Match 100.0%; Score 589; DB 10; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.9e-55;

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Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db
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61 4PCCSHV/08FFB7V4IUTCCCI DNI I CSEBDDCBVCSSMCI KNTINE 105

RESULT 12
US-09-989-721-371
Sequence 371, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730PIC55
CURRENT APPLICATION NUMBER: US/09/989, 721
CURRENT FILING DATE: 2001-11-19
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 HPGSHKVPFRKXKHTCPCLENNLCSRPDPGRYRCMDLKNINF 105

RESULT 13

US-09-992-598-371
; Sequence 371, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ahtkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04

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Patent No.. US20020172678A1			

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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLNCTPLGREGEC 60
Db 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLNCTPLGREGEC 60
QY 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRPDPGRYRCSDMLKNINF 105
Db 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRPDPGRYRCSDMLKNINF 105

Search completed: January 12, 2004, 13:40:11
Job time : 35 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:32:22 ; Search time 22 Seconds
(without alignments)
201.938 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTSQCA.....CSRFPDGRYCSMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	107.5	18.3	224	4	US-09-161-241-14
5	102	17.3	207	4	US-09-161-241-13
6	102	17.3	259	4	US-09-161-241-12
7	101	17.1	259	4	US-09-161-241-11
8	100.5	17.1	350	4	US-09-161-241-9
9	98.5	16.7	349	4	US-09-161-241-8
10	97	16.5	266	4	US-09-161-241-10
11	81	13.8	1964	4	US-09-467-997-1
12	78.5	13.3	163	2	US-08-219-237B-5
13	78.5	13.3	163	3	US-08-477-347-13
14	78.5	13.3	163	3	US-08-476-862-4
15	78.5	13.3	163	3	US-08-468-560C-5
16	78.5	13.3	163	4	US-09-800-909-4
17	75	12.7	651	1	US-08-264-101-2
18	75	12.7	651	2	US-08-765-243-2
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22	75	12.7	3075	2	US-08-460-309-5
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24	73	12.4	163	4	US-08-828-683A-13
25	73	12.4	164	2	US-08-232-087A-9
26	73	12.4	227	3	US-08-974-022-48
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32	73	12.4	235	4	US-09-326-394-4	Sequence 4, Appl
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34	73	12.4	235	4	US-09-580-235-4	Sequence 4, Appl
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45	73	12.4	257	4	US-09-579-845-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
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; Sequence 371, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P13
; CURRENT APPLICATION NUMBER: US/09/996,243
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-04-28

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.8e-59;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-712-529-5
; Sequence 5, Application US/09712529

; Patent No. 6485938
; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 105

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-712-529-5

Query Match 100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.8e-59;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEBC 60
Db |||||

QY 61 HPGSHKVPFRKRKHHTCPCLENLCSRPDPGRYRCSMDLKNINF 105

Db |||||

RESULT 3

US-09-712-529-2
; Sequence 2, Application US/09712529

; Patent No. 6485938
; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 108

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-712-529-2

Query Match 51.4%; Score 303; DB 4; Length 108;
Best Local Similarity 55.2%; Pred. No. 7.6e-27;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 10 MLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEBCHPGSHKVPF 69
Db |||||

QY 70 FRKRKHHTCPCLENLCSRPDPGRYR 96

Db |||||

QY 78 FGRMHHTCPCLENLCSRPDPGRYR 104

Db |||||

RESULT 4

US-09-161-241-14
; Sequence 14, Application US/09161241

; Patent No. 6344541
; GENERAL INFORMATION:

; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Deguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 14

; LENGTH: 224

; TYPE: PRT

; ORGANISM: Human

US-09-161-241-14

Query Match 18.3%; Score 107.5; DB 4; Length 224;

Best Local Similarity 35.5%; Pred. No. 0.00015;

Matches 22; Conservative 5; Mismatches 32; Indels 3; Gaps 1;

QY 25 ACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEBCHPGSHKVPFRKRKHHTCPCLENL 84

Db |||||

QY 144 SCLRTFDCGPGGCCARHFW---TKICKVLLLEGQVCSRGRHKDTAQAPFIFQRCDCGPG 200

Db |||||

QY 85 LC 86

Db ||

RESULT 5

US-09-161-241-13

; Sequence 13, Application US/09161241

; Patent No. 6344541
; GENERAL INFORMATION:

; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Deguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 13

; LENGTH: 207

; TYPE: PRT

; ORGANISM: Human

US-09-161-241-13

Query Match 17.3%; Score 102; DB 4; Length 207;

Best Local Similarity 31.5%; Pred. No. 0.00057;

Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVOCGAGTCCCAISLWRLGLRMCTPLGREGECC-----HPSGSHKVPFFFRKRKHTCPCL 81
DB 131 CURSSDCIEGFCARHFW---TKICKPVLHQGEVCTKQRKKGSHGLEIFOR-----CDCA 182

QY 82 PNLLCSRFDPGRY 94
DB 183 KGLSCKVWKDATY 195

RESULT 6
US-09-161-241-12
; Sequence 12, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-12

Query Match 17.3%; Score 102; DB 4; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.00074;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVOCGAGTCCCAISLWRLGLRMCTPLGREGECC-----HPSGSHKVPFFFRKRKHTCPCL 81
DB 183 CURSSDCIEGFCARHFW---TKICKPVLHQGEVCTKQRKKGSHGLEIFOR-----CDCA 234

QY 82 PNLLCSRFDPGRY 94
DB 235 KGLSCKVWKDATY 247

RESULT 7
US-09-161-241-11
; Sequence 11, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Mouse
US-09-161-241-11

Query Match 17.1%; Score 101; DB 4; Length 259;
Best Local Similarity 31.5%; Pred. No. 0.00095;
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVOCGAGTCCCAISLWRLGLRMCTPLGREGECC-----HPSGSHKVPFFFRKRKHTCPCL 81
DB 183 CLRSSDCIDGFCARHFW---TKICKPVLHQGEVCTKQRKKGSHGLEIFOR-----CDCA 234

QY 82 PNLLCSRFDPGRY 94
DB 235 KGLSCKVWKDATY 247

RESULT 8
US-09-161-241-9
; Sequence 9, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Human
US-09-161-241-9

Query Match 17.1%; Score 100.5; DB 4; Length 350;
Best Local Similarity 37.7%; Pred. No. 0.0015;
Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;

QY 26 CERDVOCGAGTCCCAISLWRLGL--RMCTPLGREGECH-PGSHKVPFFFRKRKH-----HT 77
DB 208 CQNQRDCQGLCAFAQ---RGLLPVCTPLPVEGELCHDPASRLDLITWELEPGALDR 264

QY 78 CFCPLNLLC 86
DB 265 CFCASGLLC 273

RESULT 9
US-09-161-241-8
; Sequence 8, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Mouse
US-09-161-241-8

Query Match 16.7%; Score 98.5; DB 4; Length 349;
Best Local Similarity 37.7%; Pred. No. 0.0025;
Matches 26; Conservative 4; Mismatches 28; Indels 11; Gaps 4;

QY 26 CERDVOCGAGTCCCAISLWRLGL--RMCTPLGREGECH-PGSHKVPFFR-----KKKHTT 77
DB 208 CQNQRDCQGLCAFAQ---RGLLPVCTPLPVEGELCHDPTSQLDLITWELEPGALDR 264

QY 78 CFCPLNLLC 86
DB 265 CFCASGLLC 273

RESULT 10

US-09-161-241-10
; Sequence 10, Application US/09161241
; Patent No. 6344541

; GENERAL INFORMATION:

; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daquan
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human

US-09-161-241-10

Query Match 16.5%; Score 97; DB 4; Length 266;
Best Local Similarity 32.3%; Pred. No. 0.0028;
Matches 21; Conservative 9; Mismatches 23; Indels 12; Gaps 3;

QY 26 CERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEEC---HPGSHKVPFFRKHKHTCPCL 81

DB 189 CLRSSDCASGLCCARHFV---SKICKPVLKESQVCTKHKRGSHGLEIFOR-----CYCG 240

QY 82 PNLLC 86

DB 241 EGLSC 245

RESULT 11

US-09-467-997-1
; Sequence 1, Application US/09467997
; Patent No. 6379925

; GENERAL INFORMATION:

; APPLICANT: Kitajewski, Jan
; APPLICANT: Uytendaele, Hendrik
; TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION
; FILE REFERENCE: 53863-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/467,997
; CURRENT FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1964
; TYPE: PRT
; ORGANISM: mouse

US-09-467-997-1

Query Match 13.8%; Score 81; DB 4; Length 1964;
Best Local Similarity 30.4%; Pred. No. 1.6;
Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;

QY 26 CERDVQ-----CGAGTCCCAISLWLRGLRMC-TPLGREGECHPGSHKVPFFRKHH 76

DB 188 CERDINECFLEPGPCPGTSCNTL---GSYQCLCFVQGEQPC-----KLRKG 233

QY 77 TCP---CLPNLLCSRFPDG 92

DB 234 ACPGSCCLNGTCLVPEG 252

RESULT 12

US-08-219-237B-5
; Sequence 5, Application US/08219237B
; Patent No. 5874546

; GENERAL INFORMATION:

; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto

; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James W. Hellwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/219,237B

; FILING DATE: 28-MAR-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/872,129

; FILING DATE: 22-APR-1992

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: James W. Hellwege

; REGISTRATION NUMBER: 28,808

; REFERENCE/DOCKET NUMBER: 516762

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 163 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-219-237B-5

Query Match 13.3%; Score 78.5; DB 2; Length 163;
Best Local Similarity 30.4%; Pred. No. 0.19;
Matches 28; Conservative 7; Mismatches 30; Indels 27; Gaps 5;

QY 17 SDCAVITGACERD---VQCGAGTCCCAISLWLRGLRMCTPL-----GREGE----- 59

DB 63 SDDQVETACTREQNRICTRPGWYCALSK-OEGRLCAPURKKCRPGFVGVARPGTETSDV 121

QY 60 ---CHPGSHKVPFFRKHKHTCPCLPNLLCS 87

DB 122 VKKPCAPT-----FSNTTSSDTCRPHQICN 148

RESULT 13

US-08-477-347-13
; Sequence 13, Application US/08477347
; Patent No. 6232446

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; APPLICANT: BIGDA, Jacek

; APPLICANT: BELETSKY, Igor

; APPLICANT: METT, Igor

; TITLE OF INVENTION: TNF LIGANDS

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,347

```

; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-476-862--4

Query Match 13.3% Score 78.5; DB 3; Length 163;
Best Local Similarity 30.4%; Pred. No. 0.19;
Matches 28; Conservative 7; Mismatches 30; Indels 27; Gaps 5

QY 17 SDCAVITGACRD-----VQCAGTCCALISLWLRGRLMCTPL-----GREGEE----- 59
DB 63 SDQVETQACTREONRICTCRPGWYCALSK-QEGRLCAPLRKCRPGFVGARPGTETSDV 121
QY 60 ----CHPGSHKVPFFRKRRKHHKTCPLNLLCS 87
DB 122 VCRKAPGT-----FSNTTSTDICRPHQICN 148

RESULT 15
US-08-468-560C-5
; Sequence 5, Application US/08468560C
; Patent No. 6270998
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,560C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR., GERLAD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 20-4393P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```



```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-560C-5

Query Match      13.3%; Score 78.5; DB 3; Length 163;
Best Local Similarity 30.4%; Pred. No. 0.19; 30; Indels 27; Gaps 5;
Matches 28; Conservative 7; Mismatches 30; Indels 27; Gaps 5;

QY 17 SDCAVITGACERD---VQCGAGTCCCAISLWLRGLRMCTPL-----GREGE----- 59
Db 63 SDDQVETQACTREQNRICTRPGWYCALSK-QEGCCLCAPLRKCRPGFGVARGTETSDV 121

QY 60 ----CHPGSHKVFFFRKRKHTCPCLPILLCS 87
Db 122 VCKPCAPGT-----FSNTTSTDICRPHQICN 148
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Search completed: January 12, 2004, 13:35:06
Job time : 23 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:39:28 ; Search time 20 seconds
(without alignments)
504.886 Million cell updates/sec

Title: US-10-027-603-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTSDC.....CSRFPDGRYRCMDLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 41216

Minimum DB seq length: 0

Maximum DB seq length: 105

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	10.7	95	1 XLP62	colipase II precu
2	62	10.5	92	1 S3658	proteinase inhibit
3	61.5	10.4	83	2 T28545	hypothetical prote
4	61	10.4	93	2 JE0159	gibberellin-stimul
5	61	10.4	95	2 S53510	pancreatic colipas
6	61	10.4	95	2 T42112	hypothetical prote
7	60.5	10.3	90	2 S69487	bombyxin B-7 precu
8	60.5	10.3	96	2 C86649	hypothetical prote
9	60.5	10.3	99	2 S60231	gibberellin-regula
10	60	10.2	102	2 S26409	protein 108 precu
11	59	10.0	96	2 S14018	hypothetical prote
12	58	9.8	46	2 A44794	antimicrobial pept
13	57	9.7	98	2 A75393	conserved hypothet
14	55.5	9.4	99	2 S40012	fill protein - gar
15	54.5	9.3	57	2 C46654	growth modulatory
16	54.5	9.3	63	2 S08572	chymotrypsin/elast
17	54.5	9.3	90	2 S69488	bombyxin B-7 precu
18	54.5	9.3	92	2 D37057	epithelial cell gl
19	54.5	9.3	103	4 S59331	hypothetical prote
20	53.5	9.1	57	2 A46654	growth modulatory
21	53.5	9.1	96	2 S43910	gibberellin-regula
22	53	9.0	47	2 B58319	gamma-zeathionin 2
23	53	9.0	64	2 A25775	metallothionein A
24	53	9.0	77	2 S29563	endothelin 2 precu
25	52.5	8.9	70	2 A55824	drosomycin precurs
26	52.5	8.9	77	2 S47158	metallothionein II
27	52.5	8.9	99	2 S60230	gibberellin-regula
28	52.5	8.9	101	2 C35834	isocitrate dehydro
29	52	8.8	75	1 GSFF8	salivary glue prot

ALIGNMENTS

RESULT 1

XLP62

colipase II precursor - pig

N:Alternate names: procolipase II

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 24-Apr-1984 #sequence_revision 04-Dec-1986 #text_change 26-Apr-1996

C:Accession: A03162; A90593

R:Sternby, B.; Engstrom, A.; Hellman, U.; Viher, A.M.; Sternby, N.H.; Borgstrom, B.

Biochim. Biophys. Acta 784, 75-80, 1984

A:Title: The primary sequence of human pancreatic colipase.

A:Reference number: A90652; MUID:84104937; PMID:6691986

A:Accession: A03162

A:Molecule type: protein

A:Residues: 1-95 <SR>

R:Charles, M.; Erlanson, C.; Bianchetta, J.; Joffre, J.; Guidoni, A.; Rovey, M.

Biochim. Biophys. Acta 359, 186-197, 1974

A:Title: The primary structure of porcine colipase II. I. The amino acid sequence.

A:Reference number: A90593; MUID:74290109; PMID:4859821

A:Accession: A90593

A:Molecule type: protein

A:Residues: 6-91 <CHA>

R:Erlanson, C.; Charles, M.; Astier, M.; Desnuelle, P.

Biochim. Biophys. Acta 359, 198-203, 1974

A:Title: The primary structure of porcine colipase II. II. The disulfide bridges.

A:Reference number: A90594; MUID:74290110; PMID:4603223

C:Contents: annotation; disulfide bonds

C:Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 sto

se the enzyme is washed off by bile salts, which are known to have an inhibitory effect

C:Comment: Residues 6-9 and Arg-92 are considered essential for the function of colipas

C:Superfamily: colipase

C:Keywords: lipid digestion; lipid hydrolysis; pancreas

F:1-5/Domain: propeptide #status experimental <PRO>

F:6-95/Product: colipase II #status experimental <MAR>

F:17-87,23-39,27-63,28-61,49-69/Disulfide bonds: #status experimental

F:52,55,58,59/Binding site: micellar substrate (Phe, Tyr, Tyr, Tyr) #status predicted

Query Match 10.7%; Score 63; DB 1; Length 95;

Best Local Similarity 28.8%; Pred. No. 18;

Matches 23; Conservative 4; Mismatches 41; Indels 12; Gaps 4;

QY 26 CERDVQCAGTCAISLWLRLMCTPLGREGECHPGSHKVPFFPKRKHHTCPCLPNLL 85

Db 17 CLNSAQ-C-KSNCCQDHTLSLLR-CALKARENSECS-----AFTLYGVYKCPCEGLT 68

QY 86 CSRFPDGRYRCMDLKNINF 105

Db 69 C-----EGDKSLVGSITNTNF 84

RESULT 2

S36658

proteinase inhibitors precursor (validated) - migratory locust

9 kDa-Cysteine-ric
cysteine rich oute
cellular disintegr
hypothetical prote
Na+-channel-blocki
85K MRX-20 recogni
small cysteine-ric
gamma-thionin Si-a
metallothionein -
hypothetical 90 pr
LIM1 protein - tru
cellular disintegr
Na+-channel-blocki
colipase B precurs
hypothetical prote
hypothetical prote

N:Alternate names: deoxyhexose-linked peptide; pars intercerebralis major peptide C (PMR)
N:Contains: chymotrypsin inhibitor I; chymotrypsin inhibitor II
C:Species: Locusta migratoria (migratory locust)
C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 15-Sep-2000
C:Accession: S36658; S23076; S23074; JCI1363; JCI1364
R:Laqueux, M.L.
submitted to the EMBL Data Library, May 1993
A:Reference number: S36658
A:Accession: S36658
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <LAG>
A:Cross-references: EMBL:Z22805; NID:g397613; PIDN:CAA80462.1; PID:g397614
R:Nakamura, N.; Hietter, H.; van Dorsselaer, A.; Luu, B.
Eur. J. Biochem. 204, 147-153, 1992
A:Title: Isolation and structural determination of three peptides from the insect Locusta
A:Reference number: S23074; MUID:92155197; PMID:1740125
A:Accession: S23076
A:Molecule type: protein
A:Residues: 20-54 <NAKI>
A:Accession: S23074
A:Molecule type: protein
A:Residues: 57-92 <NAK2>
A:Note: The covalently bound sugar is identified as the deoxyhexose fucose
R:Boisgrain, R.A.; Matras, H.; Brehelin, M.; Paroutaud, P.; Coletti-Previero, M.A.
Biochem. Biophys. Res. Commun. 189, 790-793, 1992
A:Title: Insect immunity: Two proteinase inhibitors from hemolymph of Locusta migratoria
A:Reference number: JCI1363; MUID:93112047; PMID:1472051
A:Accession: JCI1363
A:Molecule type: protein
A:Residues: 20-54 <BOII>
A:Accession: JCI1364
A:Molecule type: protein
A:Residues: 57-92 <BOI2>
R:Mer, G.; Hietter, H.; Lefevre, J.F.
submitted to the Brookhaven Protein Data Bank, September 1995
A:Reference number: A66384; PDB:1PMC
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R:Mer, G.; Kellenberger, C.; Koehl, P.; Stote, R.; Sorokine, O.; Van Dorsselaer, A.; Luu
Biochemistry 33, 15397-15407, 1994
A:Title: Solution structure of PMP-D2, a 35-residue peptide isolated from the insect Loc
A:Reference number: A56290; MUID:95101633; PMID:7803403
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR; chemica
R:Mer, G.; Hietter, H.; Kellenberger, C.; Renatus, M.; Luu, B.; Lefevre, J.F.
J. Mol. Biol. 238, 158-171, 1996
A:Title: Solution structure of PMP-C, a new fold in the group of small serine proteinase
A:Reference number: A58596; MUID:96200987; PMID:8613985
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
C:Comment: These proteinase inhibitors probably act in the hemolymph to inhibit interned
C:Superfamily: locust proteinase inhibitors precursor
C:Keywords: duplication; glycoprotein; hemolymph; serine proteinase inhibitor
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-54/Product: chymotrypsin inhibitor I #status experimental <MAT1>
F:57-92/Product: chymotrypsin inhibitor II #status experimental <MAT2>
F:23-38, 33-51, 36-46, 60-75, 70-89, 73-84/Disulfide bonds: #status experimental
F:65/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 10.5%; Score 62; DB 1; Length 92;
Best Local Similarity 29.6%; Pred. No. 23;
Matches 21; Conservative 6; Mismatches 38; Indels 6; Gaps 2;
QY 10 MLLLVTVSDCAVITGACERDVQCGAGTCCAIISLWGLRMCTPLGRGECHPGSHKVPF 69
DB 11 VLLVLLVQAEKCTPGVQKQDCNTCTCTPTGVMGTRKGCQAKRE-ISCPEGK----- 64
QY 70 FRKKKHHTCP 80
DB 65 TFKDKCNTCRC 75

RESULT 3
T26545
hypothetical protein YIA5A.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26545
R:Barlow, K.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z20228
A:Accession: T26545
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-83 <WIL>
A:Cross-references: EMBL:AL021177; PIDN:CAA15979.1; GSPDB:GN00021; CESP:YIA5A.2
A:Experimental source: clone YIA5A
C:Genetics:
A:Gene: CESP:YIA5A.2
A:Map position: 3
A:Introns: 27/2

Query Match 10.4%; Score 61.5; DB 2; Length 83;
Best Local Similarity 37.5%; Pred. No. 23;
Matches 18; Conservative 1; Mismatches 10; Indels 19; Gaps 3;
QY 36 TCCAIISLWGLRMCTPLGRGECHPGSHKVPFRRKKHHTCPCLP 82
DB 48 TCCICISL-----GASAPTRSPRPV----RKQHTAPSP 77

RESULT 4
JEO159
gibberellin-stimulated transcript 1 like protein - rice
N:Alternate names: GASR1
C:Species: Oryza sativa (rice)
C:Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 13-Sep-1998
C:Accession: JEO159
R:Ikeda, A.; Yamaguchi, J.; Futsuhara, Y.
Rice Genet. Newsl. 14, 150-152, 1997
A:Title: Characterization and expression of GASR1, a root-specific GAST1-like protein in
A:Reference number: JEO159
A:Accession: JEO159
A:Molecule type: mRNA
A:Residues: 1-93 <IKE>
A:Cross-references: DBJ:D15611
C:Superfamily: gibberellin-regulated protein GASA2

Query Match 10.4%; Score 61; DB 2; Length 93;
Best Local Similarity 24.3%; Pred. No. 29;
Matches 25; Conservative 11; Mismatches 23; Indels 44; Gaps 7;
QY 5 TRVSIMLLLVTVSDCAVIT-----GACERDVQCG-----AGTCCAIISLWLR 45
DB 7 TTLALLLLLLLASSLSQVSMAGSDFCGKCK--VRCASKASRHDDCLKYCGVCCASC----- 60
QY 46 GLRMCTPLGRG--RECHPGSHKVPFPR-----KKKHHTCP 79
DB 61 ---NCVPSGTAGNKDEC-----PCYRDMTTTGHGARKRPKCP 93

RESULT 5
S53510
pancreatic colipase - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S53510
R:Rugani, N.; Carriere, F.; Thim, L.; Borgstrom, B.; Sarda, L.
Biochim. Biophys. Acta 1247, 185-194, 1995
A:Title: Lipid binding and activating properties of porcine pancreatic colipase split a
A:Reference number: S53510; MUID:95210311; PMID:7696307
A:Accession: S53510
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-95 <RUG>
C:Superfamily: colipase

Query Match 10.4%; Score 61; DB 2; Length 95;

Best Local Similarity 27.5%; Pred. No. 29;
Matches 22; Conservative 4; Mismatches 42; Indels 12; Gaps 4;
QY 26 CERDQCGAGTCCCAISLWLRGLRMCPTPLGREGECHPGSHKVPFFRKXHTCCPLPNLL 85
Db 17 CLNSAQK-KSNCCQHDITL-SLSRCALKARENSECS-----AFTLYGVYKPCPCRGILT 68
QY 86 CSRFPGDGRYRCSDMLKNINF 105
Db 69 C-----EGDKSLVGSITNTNF 84

RESULT 6
T42112
hypothetical protein L7012 - Escherichia coli plasmid p0157
C:Species: Escherichia coli
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T42112
R:Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A:Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli O157:H7
A:Reference number: Z22068; MUID:98391744; PMID:9722640
A:Accession: T42112
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-95 <BUR>
A:Cross-references: EMBL:AF074613; PIDN:AAC70080.1
A:Experimental source: strain EDL933; serotype O157:H7
C:Genetics:
A:Genome: plasmid p0157
A:Note: L7012

Query Match 10.4%; Score 61; DB 2; Length 95;
Best Local Similarity 26.1%; Pred. No. 29;
Matches 12; Conservative 9; Mismatches 19; Indels 6; Gaps 1;
QY 5 TRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMC 50
Db 26 TRISLVFMVYIYVFC-----EPRQCSHSPCCVMKFRNGYRVC 65

RESULT 7
S69487
bombyxin B-7 precursor - silkworm (strain Showa)
C:Species: Bombyx mori (silkworm)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S69487; J00832
R:Kondo, H.; Ino, M.; Suzuki, A.; Ishizaki, H.; Iwami, M.
J. Mol. Biol. 259, 926-937, 1996
A:Title: Multiple gene copies for bombyxin, an insulin-related peptide of the silkworm Bombyx mori
A:Reference number: S69477; MUID:96266490; PMID:8683595
A:Accession: S69487
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-90 <KON>
A:Cross-references: EMBL:D00783; NID:g217239; PIDN:BAA00679.1; PID:g217240
A:Experimental source: strain Showa
C:Genetics:
A:Gene: bxb7
C:Superfamily: insulin
C:Keywords: pyroglutamic acid
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-46,70-90/Product: bombyxin B-7 #status predicted <MAT>
F:42-46/Domain: chain B #status predicted <BCH>
F:49-66/Domain: connecting peptide #status predicted <CP>
F:70-90/Domain: chain A #status predicted <ACH>
F:23/Modified site: pyroglutamic acid (Gln) (in mature form) #status predicted
F:30-76,42-89,75-80/Disulfide bonds: #status predicted

Query Match 10.3%; Score 60.5; DB 2; Length 90;
Best Local Similarity 27.4%; Pred. No. 32;
Matches 26; Conservative 11; Mismatches 35; Indels 23; Gaps 4;
QY 6 RVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCPTPLGREGECHPGSH 65
Db 3 KTSVMLMLV-----VVISLCSGEAEVARTYCGRHADTLADLCF-----GVKESGAQ 52
QY 66 KVPFPRKXKH-----HTC--PCLPNLLCS 87
Db 53 YAPYFTWQHGLNKGKRGVGVDECCFRPCTLDVLLS 87

RESULT 8
C86649
hypothetical protein ybJD [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86649
R:Botolin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, S.
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86649
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <STO>
A:Cross-references: GB:AE005176; PID:g12723049; PIDN:AAK04293.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ybJD

Query Match 10.3%; Score 60.5; DB 2; Length 96;
Best Local Similarity 33.3%; Pred. No. 33;
Matches 20; Conservative 4; Mismatches 19; Indels 17; Gaps 4;
QY 41 SLWLRGLRMCPTLGR-----EGESCH-PGSHKVPFPRK-----RKHHTCPCLPNLL 85
Db 21 SAWGCGFFSCLPLGFAVAVVRRRLKCHAPGCHQIGLHRTADGLYVLCRKH--PDVFNLL 78

RESULT 9
S60231
gibberellin-regulated protein GAS3 precursor - Arabidopsis thaliana
N:Alternate names: GASTI protein homolog
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 24-Sep-1999
C:Accession: S60231
R:Herzog, M.; Dorne, A.M.; Grellet, F.
Plant Mol. Biol. 27, 743-752, 1995
A:Title: GAS3, a gibberellin-regulated gene family from Arabidopsis thaliana related to gibberellin-regulated protein GAS3
A:Reference number: S60229; MUID:95244835; PMID:7727751
A:Accession: S60231
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-99 <HER>
A:Cross-references: EMBL:U11764; NID:g887934; PIDN:AAB06308.1; PID:g887935
C:Genetics:
A:Gene: GAS3
C:Superfamily: gibberellin-regulated protein GAS2
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-99/Product: gibberellin-regulated protein GAS3 #status predicted <MAT>

Query Match 10.3%; Score 60.5; DB 2; Length 99;
Best Local Similarity 23.5%; Pred. No. 34;
Matches 27; Conservative 9; Mismatches 34; Indels 45; Gaps 7;
QY 6 RVSIMLLV-----TVSDCAVITGACERDVQCGA---GTCCAIS---LWLRL 47
Db 5 RSTLVLLILFCLTTFLFVHAEDSQVGEVVK--IDCGRCRCKRSKSRPNLCRLAC 62
QY 48 RM-----CTPLGREGECHPGSHKVPFPRKXHTCCPLPNLLCSRPDGRYRC 96
Db 63 NSCCYRCNCVPPGTAG-----NHLCPCYASITTR---GGRKLC 98

```
RESULT 10
S26409
protein 108 precursor - tomato
C:Species: Lycopersicon esculentum (tomato)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C:Accession: S26409
R:Chen, R.; Smith, A.G.
submitted to the EMBL Data Library, July 1992
A:Description: Nucleotide sequence and expression of a stamen- and tapetum-specific gene
A:Reference number: S26409
A:Accession: S26409
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <CHE>
A:Cross-references: EMBL:Z14088; NID:g19151; PID:g19152

Query Match      10.2%; Score 60; DB 2; Length 102;
Best Local Similarity 25.5%; Pred. No. 39;
Matches 25; Conservative 7; Mismatches 30; Indels 36; Gaps 5;

QY 9 IMLLLVSDCAVITGACERDVCGAGTCCALSILWGLRMCTPLGREGE-----ECHPG 63
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 LLILLIVLQSQVI--ECQPQOQCTAS-----LTGLNVCAFLVPGSPSTASTCCNA 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 64 SHKVPFFRKRGKHTCP-----LPNLICS 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 VOSI-----NHDGMCNTWRIAQAQIPACNLPPLSCS 100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
S14018
hypothetical protein 16 - Chlamydomonas reinhardtii transposon
C:Species: Chlamydomonas reinhardtii
C>Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
C:Accession: S14018
R:Day, A.; Rochaix, J.D.
Nucleic Acids Res. 19, 1259-1266, 1991
A:Title: A transposon with an unusual LTR arrangement from Chlamydomonas reinhardtii con
A:Reference number: S14018; MUID:91232906; PMID:1851555
A:Accession: S14018
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <DAY>
A:Cross-references: EMBL:X56231; NID:g18229; PIDN:CAA39680.1; PID:g1360715
C:Genetics:
A:Mobile element: transposon

Query Match      10.0%; Score 59; DB 2; Length 96;
Best Local Similarity 31.2%; Pred. No. 47;
Matches 20; Conservative 7; Mismatches 23; Indels 14; Gaps 5;

QY 32 CGAGT-CCALSILW-LRGLR--MCTPLGREGECHPGSHKVPFFRKRGKHTCP-----CLPN 83
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 CAAGNGLRALASMTERRVRVLMIRPVRRKQRAPH-----PCFMDNSRHTCPYDVTCVQP 57
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 84 LLCSS 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 ATAS 61
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
A44794
antimicrobial peptide enAP-1 - horse (fragment)
C:Species: Equus caballus (domestic horse)
C>Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-1995
C:Accession: A44794; A40833
R:Couto, M.A.; Harwig, S.S.; Cullor, J.S.; Hughes, J.P.; Lehrer, R.I.
Infect. Immun. 60, 3065-3071, 1992
A:Title: Identification of enAP-1, an antimicrobial peptide from equine neutrophils.
A:Reference number: A44794; MUID:92347972; PMID:1639474
A:Accession: A44794
A>Status: preliminary
A:Molecule type: protein
```

```
A:Residues: 1-46 <COU>
A:Experimental source: neutrophils
A>Note: sequence extracted from NCBI backbone (NCBIP:109730)
C:Superfamily: granuln

Query Match      9.8%; Score 58; DB 2; Length 46;
Best Local Similarity 33.3%; Pred. No. 32;
Matches 17; Conservative 3; Mismatches 23; Indels 8; Gaps 2;

QY 29 DVQCAGTCCALSILWGLRMCTPLGREGECHPGSHKVPFFRKRGKHTCP 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DVQCGEGHFC-----HDXQTCCRASQGGXACCPYSQGVCCADQR--HCCP 43
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
A75393
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75393
R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75393
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WHI>
A:Cross-references: GB:AE001990; GB:AE000513; NID:g6459214; PIDN:AAF11024.1; PID:g64592
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1455
A:Map position: 1

Query Match      9.7%; Score 57; DB 2; Length 98;
Best Local Similarity 28.9%; Pred. No. 76;
Matches 22; Conservative 7; Mismatches 21; Indels 26; Gaps 3;

QY 2 RGATRVSIMLL-----LTVSDCAVITGACERDVCGAGTCCALSILWGLRMCTP 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24 RSEERRSVMTLASQFDNLPKLLKVSEVADFTGTHTVR-----RWIKD----- 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 53 LGREGEGCHPGSHKVP 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 -GRLGAVEHPHSLRVP 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
S40012
fill protein - garden snapdragon
C:Species: Antirrhinum majus (garden snapdragon)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000
C:Accession: S40012; S17699
R:Nacken, W.K.F.
submitted to the EMBL Data Library, January 1991
A:Reference number: S40012
A:Accession: S40012
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <NAC>
A:Cross-references: EMBL:X57296; NID:g406308; PID:g406309
R:Nacken, W.K.F.; Huijser, P.; Beltran, J.P.; Siedler, H.; Sommer, H.
Mol. Gen. Genet. 229, 129-136, 1991
A:Title: Molecular characterization of two stamen-specific genes, tap1 and fill, that a
A:Reference number: S17698; MUID:91375441; PMID:1680216
A:Accession: S17699
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91, 'AN' <NA2>
C:Genetics:
A:Gene: fill
```

A; Introns: 92/1

	Query Match	9.4%	Score 55.5;	DB 2;	Length 99;
	Best Local Similarity	28.6%;	Pred. No. 1.1e+02;		
	Matches 24;	Conservative 7;	Mismatches 42;	Indels 11;	Gaps 3;
Qy	7	VSIMLLVTVSDCAVITGACERDVQCGAGTCCALISLWLRGMRCTPLGRGEECHCPGSHK	66		
Db	8	VPLVMLTVLVAQSOLIT-----QSEAQTCSAS---LANLNACAPFVVLGAATTPSSDC	57		
Qy	67	VPFPRKRRKHHITCPLPNLLCSRFP	90		
Db	58	CTALOS--VDHECLNLTNRIASRVP	80		

RESULT 15

growth modulatory factor granulin-3 - common carp
C:Species: Cyprinus carpio (common carp)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
C:Accession: C46654; C40180
R:Belcourt, D.R.; Lazure, C.; Bennett, H.P.
J. Biol. Chem. 288, 9230-9237, 1993
A:Title: Isolation and primary structure of the three major forms of granulin-like peptide
A:Reference number: A46654; MID:93252781; PMID:8486624
A:Accession: C46654
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-57 <BEL>
A:Experimental source: spleen and head kidney
A>Note: sequence extracted from NCBI backbone (NCBIP:131316)

Query Match	9.38	Score	54.5	DB	2	Length	57
Best Local Similarity	32.5%	Pred.No.	87				
Matches	13	Conservative	6	Mismatches	18	Indels	3
Gaps							2

Search completed: January 12, 2004, 13:42:49
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 12, 2004, 13:42:19 ; Search time 33 Seconds
(without alignments)
641.167 Million cell updates/sec

Title: US-10-027-603-2
Perfect score: 589
Sequence: 1 MRGATRVISMLLVTSVDCV.....CSRFPDGRYRCSMDLKNINF 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 289840

Minimum DB seq length: 0

Maximum DB seq length: 105

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589	100.0	105	9	US-09-989-722-371
2	589	100.0	105	9	US-09-989-723-371
3	589	100.0	105	9	US-09-989-279-371
4	589	100.0	105	9	US-09-989-727-371
5	589	100.0	105	10	US-09-989-731-371
6	589	100.0	105	10	US-09-989-732-371
7	589	100.0	105	10	US-09-991-073-371
8	589	100.0	105	10	US-09-990-442-371
9	589	100.0	105	10	US-09-991-163-371
10	589	100.0	105	10	US-09-993-604-371
11	589	100.0	105	10	US-09-990-456-371
12	589	100.0	105	10	US-09-989-721-371
13	589	100.0	105	10	US-09-992-598-371
14	589	100.0	105	10	US-09-886-242A-2
15	589	100.0	105	10	US-09-989-293A-371

16	589	100.0	105	10	US-09-965-528-11	Sequence 11, Appl
17	589	100.0	105	10	US-09-989-735-371	Sequence 371, App
18	589	100.0	105	10	US-09-990-444-371	Sequence 371, App
19	589	100.0	105	10	US-09-991-181-371	Sequence 371, App
20	589	100.0	105	10	US-09-989-730-371	Sequence 371, App
21	589	100.0	105	10	US-09-990-436-371	Sequence 371, App
22	589	100.0	105	10	US-09-993-687-371	Sequence 371, App
23	589	100.0	105	11	US-09-989-734-371	Sequence 371, App
24	589	100.0	105	11	US-09-997-653-371	Sequence 371, App
25	589	100.0	105	11	US-09-993-667-371	Sequence 371, App
26	589	100.0	105	11	US-09-987-428-371	Sequence 371, App
27	589	100.0	105	11	US-09-997-666-371	Sequence 371, App
28	589	100.0	105	11	US-09-990-438-371	Sequence 371, App
29	589	100.0	105	11	US-09-990-562-371	Sequence 371, App
30	589	100.0	105	11	US-09-796-753-64	Sequence 64, Appl
31	589	100.0	105	11	US-09-990-711-371	Sequence 371, App
32	589	100.0	105	11	US-09-989-726-371	Sequence 371, App
33	589	100.0	105	11	US-09-988-156-371	Sequence 371, App
34	589	100.0	105	11	US-09-990-437-371	Sequence 371, App
35	589	100.0	105	11	US-09-991-157-371	Sequence 371, App
36	589	100.0	105	11	US-09-997-514-371	Sequence 371, App
37	589	100.0	105	11	US-09-997-573-371	Sequence 371, App
38	589	100.0	105	11	US-09-991-172-371	Sequence 371, App
39	589	100.0	105	11	US-09-990-726-371	Sequence 371, App
40	589	100.0	105	11	US-09-997-559-371	Sequence 371, App
41	589	100.0	105	11	US-09-997-601-371	Sequence 371, App
42	589	100.0	105	11	US-09-990-443-371	Sequence 371, App
43	589	100.0	105	11	US-09-991-854-371	Sequence 371, App
44	589	100.0	105	11	US-09-987-828-371	Sequence 371, App
45	589	100.0	105	11	US-09-997-683-371	Sequence 371, App

ALIGNMENTS

RESULT 1

US-09-989-722-371

; Sequence 371, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gottfredson, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730PIC63

; CURRENT APPLICATION NUMBER: US/09/989,722

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

[illegible]

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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 HPGSHKVPFRKRKHHTCCLNLLCSRPDGRYRCSMDLKNINF 105

RESULT 2
US-09-989-723-371
; Sequence 371, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1997-10-17
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;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
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Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEGATRVSTMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
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Db 61 HFGSHKVPFFRKXKHTCTCLPNLLCSRFPPDGRYRCSMDLKNINF 105
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RESULT 3
US-09-989-279-371
; Sequence 371, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24


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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MRGATRVSMILLVTVSDCAVITGACERDVQCAGTCCCAISLWLRGLRMTPLGREGERC 60
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DB      1  MRGATRVSMILLVTVSDCAVITGACERDVQCAGTCCCAISLWLRGLRMTPLGREGERC 60
      |||||||

QY      61  HPGSHKVPFRKPKHHTCPLNLLCSRPDPGRYRCMDLKNINF 105
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DB      61  HPGSHKVPFRKPKHHTCPLNLLCSRPDPGRYRCMDLKNINF 105
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RESULT 4
US-09-989-727-371
; Sequence 371, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P27301C65
; CURRENT APPLICATION NUMBER: US/09/989, 727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIIMLLLVTSVDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
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Db 1 MRGATRVSIIMLLLVTSVDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60
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QY 61 HPGSHKVPFFRRKRKHTCTCLPNLLCSRFPDGRYRCSDMLKNINF 105
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Db 61 HPGSHKVPFFRRKRKHTCTCLPNLLCSRFPDGRYRCSDMLKNINF 105
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RESULT 5
US-09-989-731-371
; Sequence 371, Application US/09989731
; Patent No. US2002010125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-04-28

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/	PRIOR FILING DATE:	1998-05-28
/	PRIOR APPLICATION NUMBER:	60/087607
/	PRIOR FILING DATE:	1998-06-02
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/	PRIOR APPLICATION NUMBER:	60/087827
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/	PRIOR FILING DATE:	1998-06-17
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MGRATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLRGEGEC 60

Qy      61 HPGSHKVPFFRRKHKHTCPCLNLLCSRFPDGRYCSMDLKNINF 105
Db      61 HPGSHKVPFFRRKHKHTCPCLNLLCSRFPDGRYCSMDLKNINF 105

RESULT 6
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; Sequence 371, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR FILING DATE: 1998-06-26
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred.No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCATISLWLRGLRMCTPLGREGSEC 60
DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCATISLWLRGLRMCTPLGREGSEC 60

QY 61 HPGSHKVPFFFRKRKHTCTCLPNLLCSRFPPDGRYRCSDMLKNINF 105
DB 61 HPGSHKVPFFFRKRKHTCTCLPNLLCSRFPPDGRYRCSDMLKNINF 105

RESULT 7
US-09-991-073-371
; Sequence 371, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db |||||
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RESULT 9
US-09-991-163-371
; Sequence 371, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991.163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
US-09-993-604-371
Sequence 371. Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Stewart, Timothy A.
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730PIC25
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46 PRIOR FILING DATE: 1998-06-26
47 PRIOR APPLICATION NUMBER: 60/091360
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56 PRIOR FILING DATE: 1998-07-02
57 PRIOR APPLICATION NUMBER: 60/091633
58 PRIOR FILING DATE: 1998-07-02
59 PRIOR APPLICATION NUMBER: 60/091978
60 PRIOR FILING DATE: 1998-07-07
61 PRIOR APPLICATION NUMBER: 60/091982
62 PRIOR FILING DATE: 1998-07-07
63 PRIOR APPLICATION NUMBER: 60/092182
64 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1,9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MRGATVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGRGEEC 60
1 MRGATVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGRGEEC 60

Qy 61 HPGSHKVPFFRRKRKHTCTCPLNLLCSRFPPDGRYRCSMDLKNINF 105
Db 61 HPGSHKVPFFRRKRKHTCTCPLNLLCSRFPPDGRYRCSMDLKNINF 105
RESULT 11
US-09-990-456-371
Sequence 371, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
 US-09-989-721-371
 ; Sequence 371, Application US/09989721
 ; Patent No. US20020142961A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tuma, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P27301C55
 ; CURRENT APPLICATION NUMBER: US/09/989,721
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 10; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.9e-55; Mismatches 0; Indels 0; Gaps 0;
Matches 105; Conservative 0;

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Db 61 HPGSHKVPFFRKRGKHTCCCLNLLCSRFPDGRYRCMDLNKINF 105

RESULT 14
US-09-886-242A-2
; Sequence 2, Application US/09886242A
; Patent No. US20020172678A1

GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William I.
TITLE OF INVENTION: EG-VEGF NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: GENENT.1516A
CURRENT APPLICATION NUMBER: US/09/886,242A
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/213,637
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PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/04914
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: PCT/US00/00219
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PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 105
TYPE: PRT
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US-09-886-242A-2

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Best Local Similarity 100.0%; Pred. No. 1.9e-55;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 HPGSHKVPFRKRKHHTCTCLPNLLCSRPDPGRYRCMDLKNINF 105

RESULT 15
US-09-989-293A-371
Sequence 371, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

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416.657 Million cell updates/sec

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	589	100.0	105 21	A human TANGO 266
2	589	100.0	105 21	Membrane-bound pro
3	589	100.0	105 22	Human PRO1186 poly
4	589	100.0	105 22	Amino acid sequenc
5	589	100.0	105 22	Human G protein-co
6	589	100.0	105 22	Human PRO1186 poly
7	589	100.0	105 22	Human PRO1186 (UNQ
8	589	100.0	105 22	Human extracellular
9	589	100.0	105 22	Human angiogenesis

10	589	100.0	105 23	AAO15527	Human physiological
11	589	100.0	105 23	AAE24382	Human prokineticin
12	589	100.0	105 23	ABB95508	Human angiogenesis
13	589	100.0	105 23	ABB06308	Human G protein-co
14	589	100.0	105 23	ABB84902	Human PRO1186 prot
15	589	100.0	105 23	AAU83674	Human PRO protein,
16	589	100.0	105 23	AAU50773	Endocrine gland-de
17	589	100.0	105 24	ABU08800	Human endocrine gl
18	589	100.0	105 24	ABU66804	Human PRO polypept
19	589	100.0	105 24	ABU67080	Human secreted/tra
20	589	100.0	105 24	ABU07603	Human ZVEN2. Homo
21	589	100.0	105 24	ABU59885	Novel secreted and
22	589	100.0	105 24	ABU59161	Novel human secret
23	589	100.0	105 24	ABU59308	Human secreted/tra
24	589	100.0	105 24	ABU59457	Novel human secret
25	589	100.0	105 24	ABU60592	Human secreted/tra
26	589	100.0	105 24	ABU58083	Human PRO polypept
27	589	100.0	105 24	ABU59014	Human secreted/tr
28	589	100.0	105 24	ABU13974	Human PRO1186 poly
29	589	100.0	105 24	ABU10929	Human PRO polypept
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31	588	99.8	105 22	AAU70147	Human G protein-co
32	588	99.8	105 23	AAU79596	GSPP4 sequence. H
33	588	99.8	105 23	AAO15526	Human physiological
34	588	99.8	105 23	ABB06307	Human G protein-co
35	588	99.8	105 24	ABP75987	Human GENSET prote
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37	586	99.5	105 21	AAU18474	A human TANGO 266
38	586	99.5	105 21	AAU18475	A human TANGO 266
39	582	98.8	105 24	ABP75986	Human GENSET prote
40	582	98.8	105 24	ABP76151	Human GENSET prote
41	545	92.5	105 23	ABU99151	Rat ZAQ protein.
42	545	92.5	105 23	ABB06956	Rat G protein-coup
43	541	91.9	105 23	ABB99153	Rat ZAQ protein.
44	541	91.9	105 23	ABB06958	Rat G protein-coup
45	539	91.5	105 23	ABB99152	Rat ZAQ protein.

ALIGNMENTS

RESULT 1
AAU18453
ID AAB18453 standard; Protein; 105 AA.

XX AAB18453;

XX 15-JAN-2001 (first entry)

XX A human TANGO 266 polypeptide.

XX TANGO 266; TANGO 261; TANGO 262; TANGO 267;
cellular proliferation; cellular differentiation; cellular adhesion;
von Willebrand factor-associated disorder; cell trafficking; cancer;
hematopoietic associated disease; atelectasis; pulmonary congestion;
oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
intestinal disorder; spleen associated disease; renal disorder;
cardiovascular disorder; ischemic heart disease; hydrocephalus;
brain herniation; iatrogenic disease; inflammation; meningitis;
Alzheimer's disease; cerebral toxoplasmosis; Parkinson's disease;
multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.

OS Homo sapiens.

XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /note= "signal sequence"
XX /note= "mature protein"

XX WO200052022-A1.

XX 08-SEP-2000.

XX 01-MAR-2000; 2000WO-US05226.
XX 01-MAR-1999; 99US-0122458.
XX (MILL-) MILLENNIUM PHARM INC.
XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
XX WPI; 2000-579269/54.
XX DR N-PSDB; AAA75155.
XX Novel human and murine secreted proteins designated TANGO 216, 261,
PT 262, 266 and 267 useful as modulating agents of cellular processes,
PT e.g. for treating cancer -
XX Claim 8; Fig 14; 175pp; English.
XX The present sequence represents a human TANGO 266 polypeptide. The
CC specification also describes TANGO 262, TANGO 216, TANGO 261, and
CC TANGO 267. The TANGO polypeptides can be used to modulate cellular
CC proliferation, modulate cellular differentiation and/or modulate
CC cellular adhesion. The proteins can be used to treat any von Willebrand
CC factor-associated disorder, regulate extracellular matrix structuring,
CC cellular adhesion, and cell trafficking and/or migration, modulate
CC cellular interactions, modulate cell adhesion in proliferative
CC disorders, such as cancer, modulate the proliferation, differentiation,
CC and/or function of cells that appear in the bone marrow, and leukocytes,
CC treat bone marrow, blood and hematopoietic associated diseases and
CC disorders, atelectasis, pulmonary congestion or oedema, emphysema,
CC chronic bronchitis, bronchial asthma and bronchiectasis, intestinal
CC disorders, spleen associated diseases, modulate renal disorders, treat
CC cardiovascular disorders such as ischemic heart disease, modulate the
CC proliferation, differentiation, and/or function of bone and cartilage
CC cells and to treat bone and/or cartilage associated diseases or
CC disorder. They may also be used to treat disorders associated with the
CC ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic
CC disease, inflammations, bacterial and viral meningitis, Alzheimer's
CC Disease, cerebral toxoplasmosis, Parkinson's disease, multiple sclerosis,
CC brain cancers, hydrocephalus and encephalitis, and treat hepatic
CC disorders.
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DB 61 HPGSHKVPFRKHKHTCPCLPNLLCSRFDPDGRYRCMDLKNINF 105
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DT 05-APR-2000 (first entry)
XX Membrane-bound protein PRO1186.
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX Homo sapiens.
XX WO9963088-A2.
PN

XX 09-DEC-1999.
PD 99WO-US12252.
XX 02-JUN-1999;
PF 98US-0087607.
XX 02-JUN-1998;
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PR	25-JUN-1998;	98US-0090690.	XX	WPI; 2000-072883/06.
PR	25-JUN-1998;	98US-0090691.	DR	N-PSDB; AAZ65091.
PR	25-JUN-1998;	98US-0090694.	XX	Membrane-bound proteins and related nucleotide sequences -
PR	25-JUN-1998;	98US-0090695.	PT	claim 12; Fig 266; 822pp; English.
PR	25-JUN-1998;	98US-0090696.	XX	The invention provides membrane-bound PRO polypeptides and
PR	26-JUN-1998;	98US-0090862.	CC	polynucleotides encoding them. The PRO sequences of the invention were
PR	26-JUN-1998;	98US-0090863.	CC	identified based on extracellular domain homology screening. The PRO
PR	01-JUL-1998;	98US-0091358.	CC	sequences have homology with proteins including LDL receptors, TIE
PR	01-JUL-1998;	98US-0091544.	CC	ligands and various enzymes. The membrane-bound proteins and receptor
PR	02-JUL-1998;	98US-0091478.	CC	molecules are useful as pharmaceutical and diagnostic agents. Receptor
PR	02-JUL-1998;	98US-0091486.	CC	immunoadhesins, for instance, can be used as therapeutic agents to block
PR	02-JUL-1998;	98US-0091519.	CC	receptor-ligand interactions. The membrane-bound proteins can also be
PR	02-JUL-1998;	98US-0091626.	CC	employed for screening of potential peptide or small molecule inhibitors
PR	02-JUL-1998;	98US-0091628.	CC	of the relevant receptor/ligand interaction. The PRO encoding sequences
PR	02-JUL-1998;	98US-0091633.	CC	are useful as hybridization probes, in chromosome and gene mapping and in
PR	02-JUL-1998;	98US-0091646.	CC	the generation of antisense RNA and DNA. PRO nucleic acid sequences
PR	07-JUL-1998;	98US-0091978.	CC	will also be useful for the preparation of PRO polypeptides, especially
PR	07-JUL-1998;	98US-0091982.	CC	by recombinant techniques.
PR	09-JUL-1998;	98US-0092182.	XX	Sequence 105 AA;
PR	10-JUL-1998;	98US-0092472.	SQ	
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PR	17-AUG-1998;	98US-0096768.		
PR	17-AUG-1998;	98US-0096773.		
PR	17-AUG-1998;	98US-0096791.		
PR	17-AUG-1998;	98US-0096867.		
PR	17-AUG-1998;	98US-0096891.		
PR	17-AUG-1998;	98US-0096894.		
PR	17-AUG-1998;	98US-0096895.		
PR	17-AUG-1998;	98US-0096897.		
PR	18-AUG-1998;	98US-0096949.		
PR	18-AUG-1998;	98US-0096950.		
PR	18-AUG-1998;	98US-0096959.		
PR	18-AUG-1998;	98US-0096960.		
PR	18-AUG-1998;	98US-0097022.		
PR	19-AUG-1998;	98US-0097141.		
PR	20-AUG-1998;	98US-0097218.		
PR	24-AUG-1998;	98US-0097661.		
PR	26-AUG-1998;	98US-0097951.		
PR	26-AUG-1998;	98US-0097952.		
PR	26-AUG-1998;	98US-0097954.		
PR	26-AUG-1998;	98US-0097955.		
PR	26-AUG-1998;	98US-0097971.		
PR	26-AUG-1998;	98US-0097974.		
PR	26-AUG-1998;	98US-0097978.		
PR	26-AUG-1998;	98US-0097979.		
PR	26-AUG-1998;	98US-0097986.		
PR	26-AUG-1998;	98US-0098014.		
PR	31-AUG-1998;	98US-0098525.		
PR	16-SEP-1998;	98US-0098525.		
PR	12-JAN-1999;	99US-0110634.		
XX		99US-0115565.		
PA	(GETH) GENENTECH INC.			
XX	Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;			
PI	Wood WI, Yuan J;			

QY	1	MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGSEC	60
Db	1	MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGSEC	60
QY	61	HPGSHKVPFFRRKHHHTCPCLPNNLLCSRFDPGRYRCSMDLKNINF	105
Db	61	HPGSHKVPFFRRKHHHTCPCLPNNLLCSRFDPGRYRCSMDLKNINF	105
RESULT	3		
AAU12406			
ID	AAU12406	standard; Protein; 105 AA.	
XX	AC	AAU12406;	
XX	AC	AAU12406;	
DT	24-OCT-2001	(first entry)	
XX	DE	Human PRO1186 polypeptide sequence.	
XX	XX	Human secretory and transmembrane; PRO; mammalian; cancer; lung;	
KW	KW	breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;	
KW	KW	cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;	
KW	KW	adipocyte; A-peptide; factor VIIA; gene therapy.	
XX	OS	Homo sapiens.	
XX	PN	WO200140466-A2.	
XX	PD	07-JUN-2001.	
XX	PF	01-DEC-2000; 2000WO-US32678.	
XX	PR	01-DEC-1999; 99WO-US28301.	
PR	PR	01-DEC-1999; 99WO-US28634.	
PR	PR	02-DEC-1999; 99WO-US28551.	
PR	PR	02-DEC-1999; 99WO-US28564.	
PR	PR	02-DEC-1999; 99WO-US28565.	
PR	PR	16-DEC-1999; 99US-0170262.	
PR	PR	16-DEC-1999; 99WO-US30095.	
PR	PR	20-DEC-1999; 99WO-US30911.	
PR	PR	20-DEC-1999; 99WO-US30999.	
PR	PR	30-DEC-1999; 99WO-US31243.	
PR	PR	06-JAN-2000; 2000WO-US00277.	
PR	PR	06-JAN-2000; 2000WO-US00376.	

PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 XX WPI; 2001-408281/43.
 DR N-PSDB; AAS21478.
 XX
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical -
 XX
 XX Claim 12; Fig 470; 813pp; English.
 PS
 XX AAU2172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 XX Sequence 105 AA;
 SQ
 Query Match 100.0%; Score 589; DB 22; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.2e-56;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGATRVSIIMLLVTVSDCAVITGACERDVQCAGTGCCCAISLWRLGLRMCTPLGREGGEC 60
 DB 1 MRGATRVSIIMLLVTVSDCAVITGACERDVQCAGTGCCCAISLWRLGLRMCTPLGREGGEC 60
 QY 61 HPGSHKVPFFRKXKHTTCPLNLLCSRPDPGRYRCMDLKNINF 105
 DB 61 HPGSHKVPFFRKXKHTTCPLNLLCSRPDPGRYRCMDLKNINF 105
 RESULT 4
 AAB68427
 ID AAB68427 standard; Protein; 105 AA.
 XX
 AC AAB68427;
 XX
 XX 23-JUL-2001 (first entry)
 DE Amino acid sequence of a human Zven2 polypeptide.
 XX
 XX Zven1; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing;
 KW antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme;
 KW cellular differentiation; gastrointestinal cell contractility;
 KW gastrointestinal motility; inflammation; hypermotility; diarrhoea;
 KW Crohn's disease.
 XX
 XX Homo sapiens.
 XX
 XX WO200136465-A2.
 XX
 XX 25-MAY-2001.
 PD
 XX 14-NOV-2000; 2000WO-US31278.
 XX
 XX 16-NOV-1999; 99US-0442164.
 PR 25-FEB-2000; 2000US-0511879.
 PR 19-APR-2000; 2000US-0552203.
 PR 07-JUN-2000; 2000US-0210332.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Sheppard PO, Bishop PD, Whitmore TE, Thompson PP;
 PI
 XX WPI; 2001-355611/37.
 DR N-PSDB; AAF85427.
 XX
 XX Novel isolated Zven polypeptide useful for inhibiting proliferation of
 PT tumour cells, for treating small cell cancer of lung, to promote wound
 PT healing, and for treating Crohn's disease and diarrhoea -
 XX
 XX Claim 27; Page 4; 98pp; English:
 The present sequence represents a human Zven2 polypeptide. The
 CC specification also describes Zven1. The Zven1 gene is present on
 CC chromosome 3p21.1-3p14.3. The specification also describes Zven2. Zven
 CC polynucleotides and polypeptides are useful in veterinary and human
 CC therapeutics, for treating small cell cancer of the lung, to promote
 CC wound healing, to prevent or to treat an adverse reaction of the skin
 CC to a skin-sensitizing agent or a skin-irritating agent, to stimulate
 CC the immune system of an immunocompromised individual, as antitumour
 CC agents, as antiinflammatory agents, as agents to regulate regeneration
 CC or remodeling of tissue, as agents to modulate necrosis or tissue
 CC growth developmental arrest, to inhibit proliferation of tumour cells,
 CC cellular differentiation and necrosis, to treat disorders associated
 CC with gastrointestinal cell contractility, secretion of digestive
 CC enzymes and acids, gastrointestinal motility, recruitment of digestive
 CC enzymes, inflammation, and conditions associated with hypermotility
 CC such as diarrhoea and Crohn's disease.
 XX
 XX Sequence 105 AA;
 SQ
 Query Match 100.0%; Score 589; DB 22; Length 105;
 Best Local Similarity 100.0%; Pred. No. 9.2e-56;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGATRVSIIMLLVTVSDCAVITGACERDVQCAGTGCCCAISLWRLGLRMCTPLGREGGEC 60
 DB 1 MRGATRVSIIMLLVTVSDCAVITGACERDVQCAGTGCCCAISLWRLGLRMCTPLGREGGEC 60
 QY 61 HPGSHKVPFFRKXKHTTCPLNLLCSRPDPGRYRCMDLKNINF 105
 DB 61 HPGSHKVPFFRKXKHTTCPLNLLCSRPDPGRYRCMDLKNINF 105
 RESULT 5
 AAB70148
 ID AAB70148 standard; Protein; 105 AA.
 XX
 XX

AC AAB70148;
XX 29-MAY-2001 (first entry)
XX Human G protein-coupled receptor protein-related sequence #4.
DE Human; G protein-coupled receptor protein; neotropic; neuroprotective;
XX hypotensive; orexigenic; anti-allergic; anti-angiogenic; antimicrobial;
KW antibacterial; gene therapy; Alzheimer's disease; hypertension;
KW anorexia; allergy; angina pectoris; infection; MRSA;
KW multiple resistant Staphylococcus aureus.
XX Homo sapiens.
OS WO200116309-A1.
XX 08-MAR-2001.
XX 24-AUG-2000; 2000WO-JP05685.
XX 27-AUG-1999; 99JP-0241531.
PR 18-JUL-2000; 2000JP-0217474.
XX (TAKA) TAKEDA CHEM IND LTD.
PA Watanabe T, Terao Y, Shintani Y;
PI WPI; 2001-226684/23.
XX New human brain-originated guanosine triphosphate protein-coupled
PT receptor protein, its salt and encoded gene, useful in (gene) diagnosis
PT and development of preventives and remedies for Alzheimer's disease,
PT hypertension and anorexia -
XX Example 4; Page 113; 119pp; Japanese.
XX The present sequence is provided in a specification relating to a
CC protein or its salt with an amino acid sequence identical or
CC substantially similar to a fully defined sequence of 393 amino acids as
CC given in the specification. The protein is useful in gene diagnosis and
CC development of preventives and remedies for diseases associated with
CC dysfunction of the protein, e.g. Alzheimer's disease, hypertension,
CC anorexia, allergy, angina pectoris and infections (e.g. multiple
CC resistant Staphylococcus aureus). The proteins and DNA encoding the
CC proteins are also useful for the treatment of these diseases by gene
CC therapy.
XX Sequence 105 AA;
SQ Query Match 100.0%; Score 589; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
Db 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFFRRKRKHHTCPCLNLLCSRFPDGRYRCSMDLKNINF 105
Db 61 HPGSHKVPFFRRKRKHHTCPCLNLLCSRFPDGRYRCSMDLKNINF 105
RESULT 6
AAB48175
ID AAB48175 standard; Protein; 105 AA.
XX AAB48175;
XX 02-APR-2001 (first entry)
XX Human PRO1186 polypeptide.
XX PRO1186; PRO184; neoplastic; cell growth; tumour; cancer; breast;

KW ovarian; renal; colorectal; uterine; prostate; lung; melanoma;
KW central nervous system; leukemia; antitumor; cytostatic.
XX Homo sapiens.
XX Location/Qualifiers
FH Key 1..19
FT Peptide /note= "signal sequence"
FT Protein 20..105
FT /note= "mature protein"
FT Modified-site 33..39
FT /note= "N-myristoylation site"
FT Modified-site 35..41
FT /note= "N-myristoylation site"
FT Modified-site 46..52
FT /note= "N-myristoylation site"
FT Modified-site 88..95
FT /note= "tyrosine kinase phosphorylation site"
XX WO200075327-A1.
XX 14-DEC-2000.
XX 24-FEB-2000; 2000WO-US04914.
XX 02-JUN-1999; 99WO-US12252.
PR 26-JUL-1999; 99US-0145698.
PR 05-JAN-2000; 2000WO-US00219.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Hallan KJ, Napier MA, Watanabe CK, Wood WI;
PI WPI: 2001-071078/08.
XX N-PSDB; AAC84469.
XX Compositions for inhibiting neoplastic cell growth and treating tumor,
PT a cancer, comprises novel PRO1186 or PRO184 polypeptides or its agonist
PT -
XX Claim 31; Fig 2; 104pp; English.
XX The invention provides PRO1186 and PRO184 polypeptides that can be used
CC for the inhibition of neoplastic cell growth and for treating tumours.
CC The PRO polypeptides can be expressed by standard recombinant
CC methodology. The PRO polypeptides or their agonists are useful for
CC inhibition of neoplastic cell growth and for treating tumours, cancers
CC such as breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder or central nervous system cancers or melanoma and leukemia. The
CC present sequence represents the human PRO1186 polypeptide (encoding
CC cDNA clone ID: DNA60621-1516).
XX Sequence 105 AA;
SQ Query Match 100.0%; Score 589; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
Db 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFFRRKRKHHTCPCLNLLCSRFPDGRYRCSMDLKNINF 105
Db 61 HPGSHKVPFFRRKRKHHTCPCLNLLCSRFPDGRYRCSMDLKNINF 105
RESULT 7
AAB65268
ID AAB65268 standard; Protein; 105 AA.
XX AAB65268;
XX

DT 02-APR-2001 (first entry)

XX Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.

DE Human; secreted and transmembrane protein; PRO; cytostatic;

XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;

KW diagnostic assay.

KW Homo sapiens.

OS WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99WO-US21090.

PR 08-OCT-1999; 99WO-US21547.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28301.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 11-FEB-2000; 2000WO-US00376.

PR 18-FEB-2000; 2000WO-US03565.

PR 22-FEB-2000; 2000WO-US04341.

PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.

PR 02-MAR-2000; 2000WO-US05841.

PR 15-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Deanovsers L, Eaton DL;

PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi CJ, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;

XX WPI; 2001-032160/04.

DR N-PSDB; AAF44237.

XX PRO polynucleotides used to produce polypeptides used to target

PT bioactive molecules such as toxins, radiolabels or antibodies, to

PT specific cells, to cause targeted cell death -

XX Claim 12; Fig 266; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO

XX proteins. The PRO proteins have cytostatic activity. The PRO proteins

CC can be used for targeted delivery of bioactive molecules, such as

CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

CC sequences, and their fragments, can be used as hybridisation probes, in

CC chromosomal and gene mapping, and in the generation of anti-sense RNA

CC and DNA. They may also be used to produce transgenic animals which are

CC used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in

CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.

CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and

CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX

SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 22; Length 105;

Best Local Similarity 100.0%; Pred. No. 9.2e-56; Indels 0; Gaps 0;

Matches 105; Conservative 0; Mismatches 0;

QY 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLRGREGEC 60

Db 1 MEGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLRGREGEC 60

QY 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRPPDGRYRCSMDLKNINF 105

Db 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRPPDGRYRCSMDLKNINF 105

RESULT 8

AA48067

ID AAB48067 standard; protein; 105 AA.

XX AAB48067;

XX 19-MAR-2001 (first entry)

XX Human extracellular signaling molecule (EXCS) (ID 2006548CD1).

XX Extracellular signaling molecule; EXCS; anti-inflammatory; human;

KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;

KW virucide; antibacterial; anti-HIV; human immunodeficiency virus;

KW antinfertility; cerebroprotective; nootropic; antitumor; antifungal;

KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;

KW keratolytic; protozoicide; gene therapy.

XX Homo sapiens.

XX WO200070049-A2.

XX 23-NOV-2000.

XX 19-MAY-2000; 2000WO-US13975.

PR 19-MAY-1999; 99US-0134949.

PR 15-JUL-1999; 99US-0144270.

PR 30-JUL-1999; 99US-0146700.

PR 04-OCT-1999; 99US-0157508.

XX (INCY-) INCYTE GENOMICS INC.

PI Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;

PI Azimzai Y, Lu DAM, Patterson C;

XX WPI; 2001-025021/03.

DR N-PSDB; AAC84303.

XX New human extracellular signaling nucleic acids and polypeptides useful

PT for diagnosing, treating and preventing infections and

PT gastrointestinal, neurological, reproductive, and

PT autoimmune/inflammatory disorders -

XX Claim 1; Page 89; 114pp; English.

XX The invention provides human extracellular signaling molecules (EXCS)

CC and polynucleotides which identify and encode EXCS. EXCS can be

CC expressed by standard recombinant methodology. The amino acid and nucleic

CC acid sequences of EXCS are useful for diagnosing, treating and

CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,

CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular

CC disease, stroke), reproductive (infertility, ovulatory defects,

CC endometriosis), autoimmune/inflammatory (actinic keratosis, acquired

CC immunodeficiency syndrome (AIDS), Addison's disease), and cell

CC proliferative disorders including cancers (of the breast, adrenal gland,

CC bone). They may also be used to treat fatal familial insomnia,

CC nutritional and metabolic diseases of the nervous system, myopathies,

CC mental disorders (anxiety, schizophrenia, mood), as well as infections

CC caused by parasites (malaria, leishmania, trypanosoma), viral
CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,
CC staphylococcus, bacillus), and fungal (aspergillus, blastomycetes,
CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,
CC agonists, pharmaceutical compositions, and antibodies may also be used
CC for treating or preventing disorders associated with increased or
CC decreased expression or activity of EXCS. EXCS polynucleotides may also
CC be used to detect and quantify gene expression in biopsied tissues in
CC which expression of EXCS may be correlated with the disease, to determine
CC presence or excess expression of EXCS, to monitor regulation of EXCS
CC levels during therapeutic intervention, to detect the presence of
CC associated disorders, as targets in microarray, to generate hybridization
CC probes, and to detect differences in gene sequences among normal, carrier
CC or affected individuals. Antibodies may also be used in diagnosing
CC disorders, in monitoring patients being treated with EXCS agonists,
CC antagonists or inhibitors. Sequences AAB48057-B48082 represent the EXCS
CC of the invention.

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRMCTPLRGEGEC 60

DB 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRMCTPLRGEGEC 60

QY 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSFPPDGRYRCSDMLKNINF 105

DB 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSFPPDGRYRCSDMLKNINF 105

RESULT 9

AAB53096

ID AAB53096 standard; Protein; 105 AA.

XX AC AAB53096;

XX DT 28-FEB-2001 (first entry)

XX DE Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.

XX KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal.

XX OS Homo sapiens.

XX PN WO200053753-A2.

XX PD 14-SEP-2000.

XX PF 05-JAN-2000; 2000WO-US00219.

XX PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 14-MAY-1999; 99US-0134287.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR

02-DEC-1999; 99WO-US28564.

XX 02-DEC-1999; 99WO-US28565.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;

PI Gadowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;

PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2001-090793/10.

DR N-PSDB; AAC97496.

XX New isolated nucleic acid for producing a PRO polypeptide, analyzing

PT genetic disorders and treating cardiovascular, endothelial or

PT angiogenic disorders, such as atherosclerosis, wounds or cancer -

XX Claim 69; Fig 66; 293pp; English.

XX The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof.
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in
CC gene therapy. PRO nucleic acids can also be used to produce transgenic
CC animals useful for the development and screening of potential
CC therapeutic agents. The present sequence represents a PRO protein of the
CC invention.

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 22; Length 105;

Best Local Similarity 100.0%; Pred. No. 9.2e-56;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRMCTPLRGEGEC 60

DB 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWLRMCTPLRGEGEC 60

QY 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSFPPDGRYRCSDMLKNINF 105

DB 61 HPGSHKVPFFFRKRKHHTCPCLPNLLCSFPPDGRYRCSDMLKNINF 105

RESULT 10

AAO15527

ID AAO15527 standard; Protein; 105 AA.

XX AC AAO15527;

XX DT 24-OCT-2002 (first entry)

XX

DE Human physiologically-active ZAQ ligand-related protein 3.
XX
KW Human; ZAQ ligand; physiologically-active ZAQ ligand;
KW digestive disease; colitis; diarrhoea.
XX
OS Homo sapiens.
XX
PN WO200257443-A1.
XX
PD 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-JP00378.
XX
PF 22-JAN-2001; 2001JP-0013027.
PR 17-MAY-2001; 2001JP-0147759.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Yamada T, Suenaga M, Nishimura O;
XX
XX WPI; 2002-566801/60.
XX

PT Industrial production of physiologically-active ZAQ ligand by
PT expressing in transformant prokaryote and refolding in redox buffer,
PT for use in preventing or treating digestive diseases e.g. colitis and
PT diarrhea -
XX
XX Example 3; Page 76-77; 93pp; Japanese.
XX
XX The invention comprises a method for producing an active peptide that has
XX the same activity as a ZAQ ligand isolated from eukaryotic cells. The
XX method of the invention is useful for the production of a
XX physiologically-active ZAQ ligand for use in preventing or treating
XX digestive diseases (e.g. colitis and diarrhea). The present amino acid
XX sequence represents a human physiologically active ZAQ ligand-related
XX protein.
XX
XX Sequence 105 AA;
SQ

Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
DB 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFPRKRKHHTCPLPCLNLLCSRPDPGRYRCMDLKNINF 105
DB 61 HPGSHKVPFPRKRKHHTCPLPCLNLLCSRPDPGRYRCMDLKNINF 105

RESULT 11
AAE24382
ID AAE24382 standard; Protein; 105 AA.
XX
AC AAE24382;
XX
DT 04-OCT-2002 (first entry)
XX
XX Human prokineticin 1 precursor protein.
XX
XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;
KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;
KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;
KW inflammatory bowel disorder; analgesic; infectious disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide 20..105

FT
XX
PN WO200236625-A2.
XX
PD 10-MAY-2002.
XX
XX 01-NOV-2001; 2001WO-US47969.
XX
PR 03-NOV-2000; 2000US-245882P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Zhou Q. Ehlert FJ;
XX
XX WPI; 2002-479752/51.
XX
XX N-PSDB; AAD39321.
XX
XX New isolated human prokineticin 1 and 2 polypeptides that stimulate
XX gastrointestinal smooth muscle contraction, useful for improving
XX impaired gastrointestinal motility in irritable bowel syndrome, chronic
XX constipation -
XX
XX Example 1; Fig 1; 86pp; English.
XX
XX The invention relates to human prokineticin 1 and 2 polypeptides that
XX stimulate gastrointestinal smooth muscle contraction and nucleic acid
XX molecules encoding such polypeptides. Polypeptides of the invention
XX are useful for treating disorders involving impaired gastrointestinal
XX motility. They are useful for stimulating gastrointestinal motility
XX in disorders such as irritable bowel syndrome, diabetic gastroparesis,
XX post-operative ileus, chronic constipation and gastrointestinal
XX reflux disease. The prokineticin antagonists are useful for inhibiting
XX gastrointestinal motility in conditions of diarrhoea, malabsorptive
XX disorders, inflammatory bowel disorders, infectious diseases and
XX intestinal cancers. The antagonists also act as analgesics. The present
XX sequence is human prokineticin 1 precursor protein.
XX
XX Sequence 105 AA;
SQ

Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
DB 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFPRKRKHHTCPLPCLNLLCSRPDPGRYRCMDLKNINF 105
DB 61 HPGSHKVPFPRKRKHHTCPLPCLNLLCSRPDPGRYRCMDLKNINF 105

RESULT 12
ABB95508
ID ABB95508 standard; Protein; 105 AA.
XX
AC ABB95508;
XX
DT 19-JUL-2002 (first entry)
XX
XX Human angiogenesis related protein PRO1186 SEQ ID NO: 172.
XX
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
XX Homo sapiens.
XX
XX WO200208284-A2.
XX
XX 31-JAN-2002.
XX

PF 09-JUL-2001; 2001WO-US21735.
XX 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000US-233328.
PR 07-SEP-2000; 2000US-230378P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 10-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US30873.
PR 20-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-171999/22.
DR N-PSDB; ABL95646.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 172; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac

CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRFPPDGRYRCSDMLKNINF 105
DB 61 HPGSHKVPFFRRKRKHHTCPLNLLCSRFPPDGRYRCSDMLKNINF 105
RESULT 13
ABB06308
ID ABB06308 standard; Protein; 105 AA.
XX
AC ABB06308;
XX
DT 27-MAY-2002 (first entry)
XX
DE Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.
XX
KW G protein-coupled receptor; ZAQ ligand; physiologically active peptide;
KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;
KW colitis; diarrhoea; constipation; poor-absorption syndrome;
KW Gene therapy.
XX
OS Homo sapiens.
XX
XX WO200206483-A1.
PN
XX
PD 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-JP06162.
XX
XX 18-JUL-2000; 2000JP-0217442.
PR 02-FEB-2001; 2001JP-0026779.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
PI Hinuma S;
XX
XX WPI; 2002-198546/24.
DR N-PSDB; ABL49637.
XX
XX Physiologically-active peptides from cows milk, useful for developing
PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases
PT like colitis, diarrhoea, constipation and poor-absorption syndrome, by
PT gene therapy -
XX
XX Claim 5; Page 61; 191pp; Japanese.
XX
XX The present invention describes a peptide containing an amino acid
CC sequence (I) identical to or substantially similar to that of the
CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic
CC and laxative activities. The peptides and encoding DNAs from the
CC present-invention are useful for developing drugs to treat digestive
CC diseases like colitis, diarrhoea, constipation and poor-absorption
CC syndrome, including gene therapy. The physiologically-active cows
CC milk-originated peptides are applicable as a specific ligand of
CC brain-originated orphan G protein-coupled receptor protein ZAQ.
CC ABL49615 to ABB40659 and ABB06303 to ABB06315 represent sequences
CC used in the exemplification of the present invention.

```
XX SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
DB 1 MEGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFFRKRGKHTCPCLEPNCSCRPDGRYRCMDLKNINF 105
DB 61 HPGSHKVPFFRKRGKHTCPCLEPNCSCRPDGRYRCMDLKNINF 105

RESULT 14
ABB84902
ID ABB84902 standard; Protein; 105 AA.
XX AC ABB84902;
XX DT 16-MAY-2002 (first entry)
XX DE Human PRO1186 protein sequence SEQ ID NO:172.
XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX OS Homo sapiens.
XX PN WO200200690-A2.
XX PD 03-JAN-2002.
XX PF 20-JUN-2001; 2001WO-US19692.
XX PR 23-JUN-2000; 2000US-213637P.
XX PR 20-JUL-2000; 2000US-219556P.
XX PR 25-JUL-2000; 2000US-220624P.
XX PR 25-JUL-2000; 2000US-220664P.
XX PR 28-JUL-2000; 2000WO-US20710.
XX PR 02-AUG-2000; 2000US-222695P.
XX PR 17-AUG-2000; 2000US-064357.
XX PR 23-AUG-2000; 2000WO-US23322.
XX PR 24-AUG-2000; 2000WO-US23328.
XX PR 07-SEP-2000; 2000US-230978P.
XX PR 18-SEP-2000; 2000US-0664610.
XX PR 18-SEP-2000; 2000US-0665350.
XX PR 24-OCT-2000; 2000US-242922P.
XX PR 08-NOV-2000; 2000US-0709238.
XX PR 08-NOV-2000; 2000WO-US30952.
XX PR 10-NOV-2000; 2000WO-US30873.
XX PR 01-DEC-2000; 2000WO-US32678.
XX PR 20-DEC-2000; 2000US-0747259.
XX PR 20-DEC-2000; 2000WO-US34956.
XX PR 22-JAN-2001; 2001US-0767609.
XX PR 28-FEB-2001; 2001US-0796498.
XX PR 28-FEB-2001; 2001WO-US06520.
XX PR 01-MAR-2001; 2001WO-US06666.
XX PR 09-MAR-2001; 2001US-0802706.
XX PR 14-MAR-2001; 2001US-0806889.
XX PR 22-MAR-2001; 2001US-0816744.
XX PR 05-APR-2001; 2001US-0828366.
XX PR 10-MAY-2001; 2001US-0854208.
XX PR 10-MAY-2001; 2001US-0854280.
XX PR 25-MAY-2001; 2001US-0866028.

25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001WO-US17092.
30-MAY-2001; 2001US-0870574.
30-MAY-2001; 2001WO-US17443.
01-JUN-2001; 2001WO-US17800.
(GETH ) GENENTECH INC.
XX PA
XX PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
XX PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX DR WPI; 2002-090516/12.
XX DR N-PSDB; ABL88157.
XX PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX PT infarction), endothelial or angiogenic disorders in a mammal -
XX PS Claim 11; Fig 172; 565pp; English.
XX CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
XX CC activities, and can be used in gene therapy. The PRO polynucleotides,
XX CC proteins, agonists and antagonists are useful for treating or diagnosing
XX CC a cardiovascular, endothelial or angiogenic disorder in a mammal.
XX CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX CC degeneration, atherosclerosis, hypertension, arterial restenosis,
XX CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX CC carcinoma) and wound healing. The PRO polynucleotides have applications
XX CC in molecular biology, including use as hybridisation probes, and in
XX CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX CC probes used in the exemplification of the present invention.
XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
DB 1 MEGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
QY 61 HPGSHKVPFFRKRGKHTCPCLEPNCSCRPDGRYRCMDLKNINF 105
DB 61 HPGSHKVPFFRKRGKHTCPCLEPNCSCRPDGRYRCMDLKNINF 105

RESULT 15
AAU83674
ID AAU83674 standard; Protein; 105 AA.
XX AC AAU83674;
XX DT 08-MAY-2002 (first entry)
XX DE Human PRO protein, Seq ID No 166.
XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX KW breast cancer; prostate tumour; rectal tumour; liver tumour;
XX KW pericyte cell proliferation; chondrocyte cell proliferation;
XX KW tumour necrosis factor-alpha.
XX OS Homo sapiens.
XX PN WO200208288-A2.
XX PD 31-JAN-2002.
XX PF 29-JUN-2001; 2001WO-US21066.
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XX 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000US-220710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI: 2002-172001/22.
DR N-PSDB; ABK33618.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
PS Claim 11; Figure 166; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 589; DB 23; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.2e-56;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MRGATRVSIIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRLMCTPLGREGEC 60
DB 1 MRGATRVSIIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRLMCTPLGREGEC 60
OY 61 HPGSHKVPFFRKHKHHTCPCLPNLLCSRFPPDGRYCSMDLKNINF 105
DB 61 HPGSHKVPFFRKHKHHTCPCLPNLLCSRFPPDGRYCSMDLKNINF 105

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